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da Costa e Silva et al.

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(54) **PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF USE IN PLANTS**

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(21) Appl. No.: **12/873,345**

(22) Filed: **Sep. 1, 2010**

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US 2010/0325759 A1 Dec. 23, 2010

Related U.S. Application Data

(60) Division of application No. 09/828,313, filed on Apr. 6, 2001, now Pat. No. 6,867,351, and a continuation of application No. 12/545,903, filed on Aug. 24, 2009, now Pat. No. 7,858,847, and a continuation of application No. 12/401,635, filed on Mar. 11, 2009, and a continuation of application No. 11/961,634, filed on Dec. 20, 2007, now Pat. No. 7,521,598, and a continuation of application No. 11/564,902, filed on Nov. 30, 2006, now Pat. No. 7,504,559, and a continuation of application No. 10/768,863, filed on Jan. 30, 2004, now Pat. No. 7,179,962.

(60) Provisional application No. 60/196,001, filed on Apr. 7, 2000.

(51) **Int. Cl.**

C12N 15/82	(2006.01)
C12N 15/29	(2006.01)
A01H 5/00	(2006.01)
A01H 5/10	(2006.01)

(52) **U.S. Cl.** **800/289**; 435/419; 536/23.6; 800/298; 800/320; 800/320.1; 800/320.2; 800/320.3; 800/312; 800/314; 800/306; 800/322; 800/313; 800/317; 800/317.1; 800/317.2; 800/317.3; 800/317.4

(58) **Field of Classification Search** ..... None
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

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* cited by examiner

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(74) *Attorney, Agent, or Firm* — Patricia A. McDaniels

(57) **ABSTRACT**

A transgenic plant transformed by a Protein Kinase Stress-Related Protein (PKSRP) coding nucleic acid, wherein expression of the nucleic acid sequence in the plant results in increased tolerance to environmental stress as compared to a wild type variety of the plant. Also provided are agricultural products, including seeds, produced by the transgenic plants. Also provided are isolated PKSRPs, and isolated nucleic acid coding PKSRPs, and vectors and host cells containing the latter.

22 Claims, 18 Drawing Sheets

Figure 1

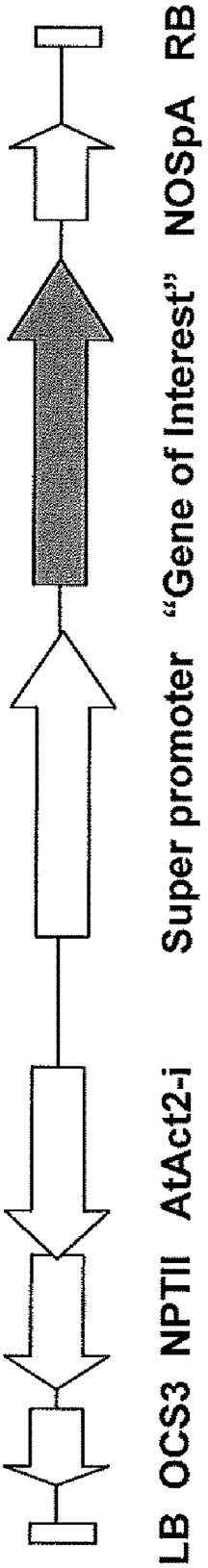
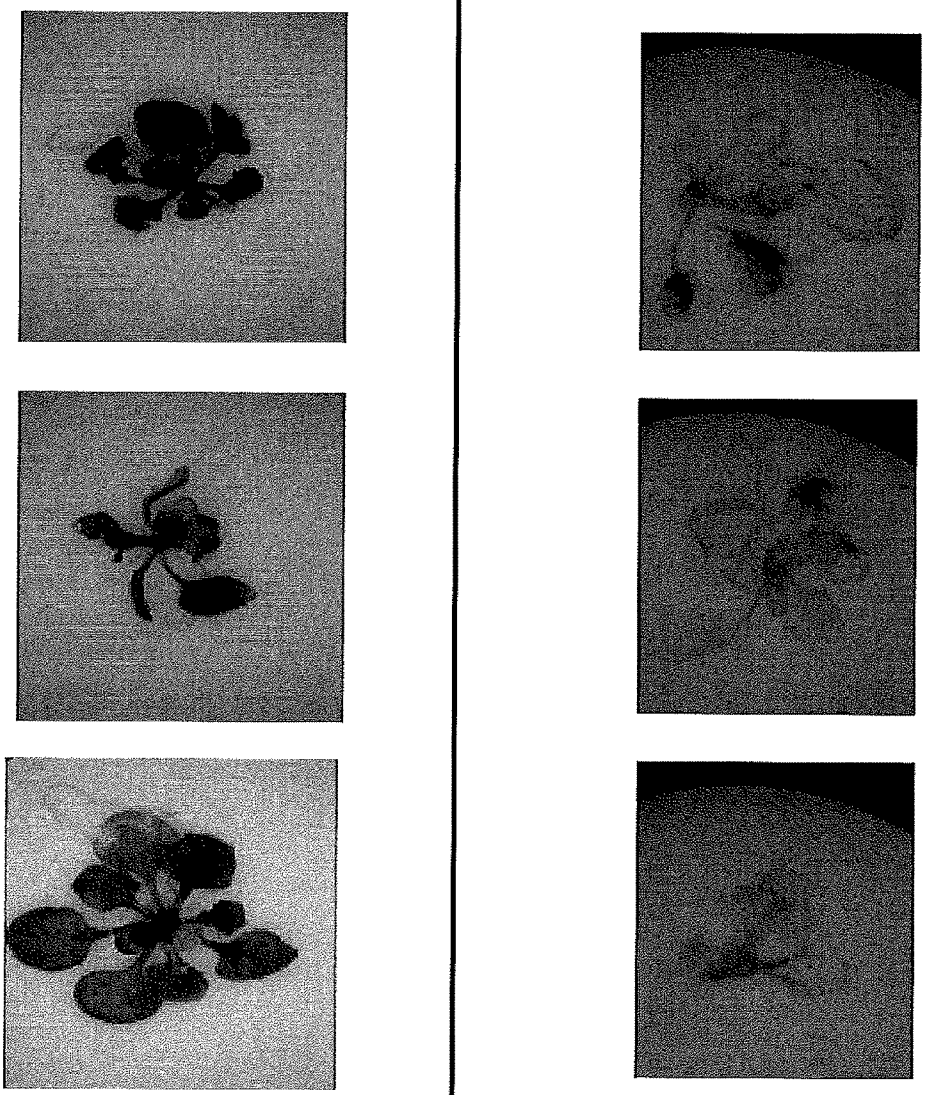

LB OCS3 NPTII AtAct2-i Super promoter "Gene of Interest" NOSpA RB

Figure 2



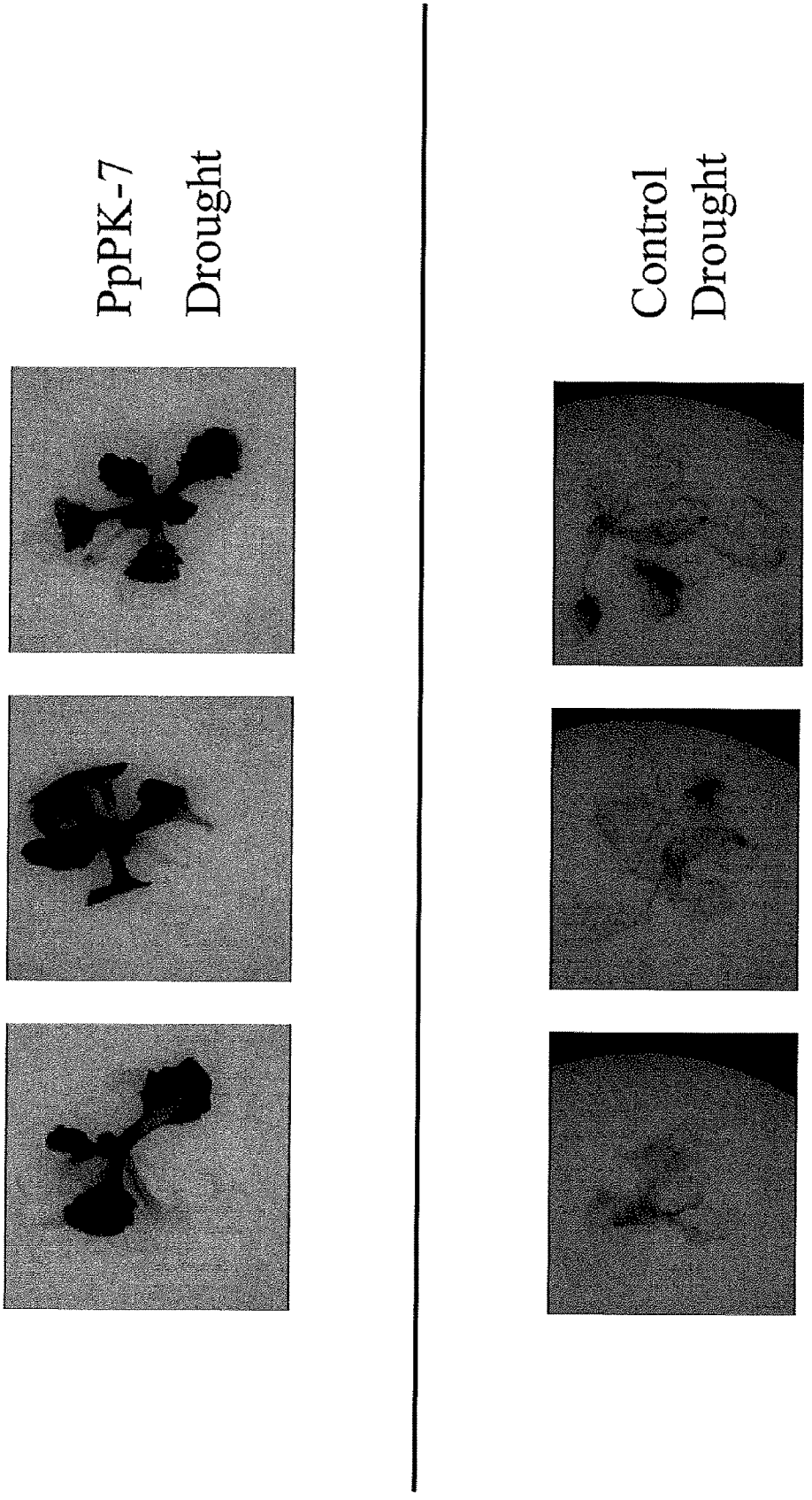
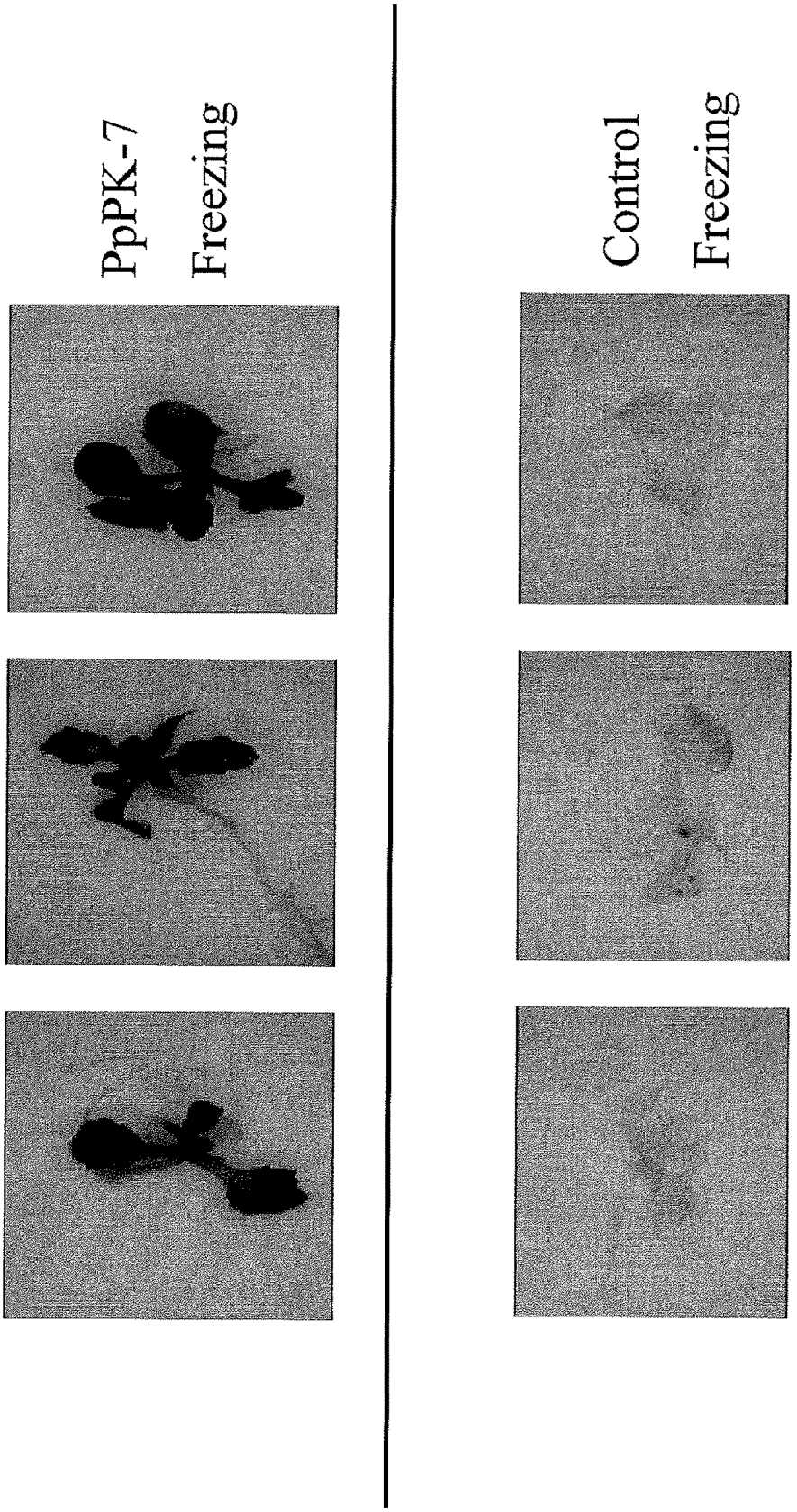


Figure 3

Figure 4



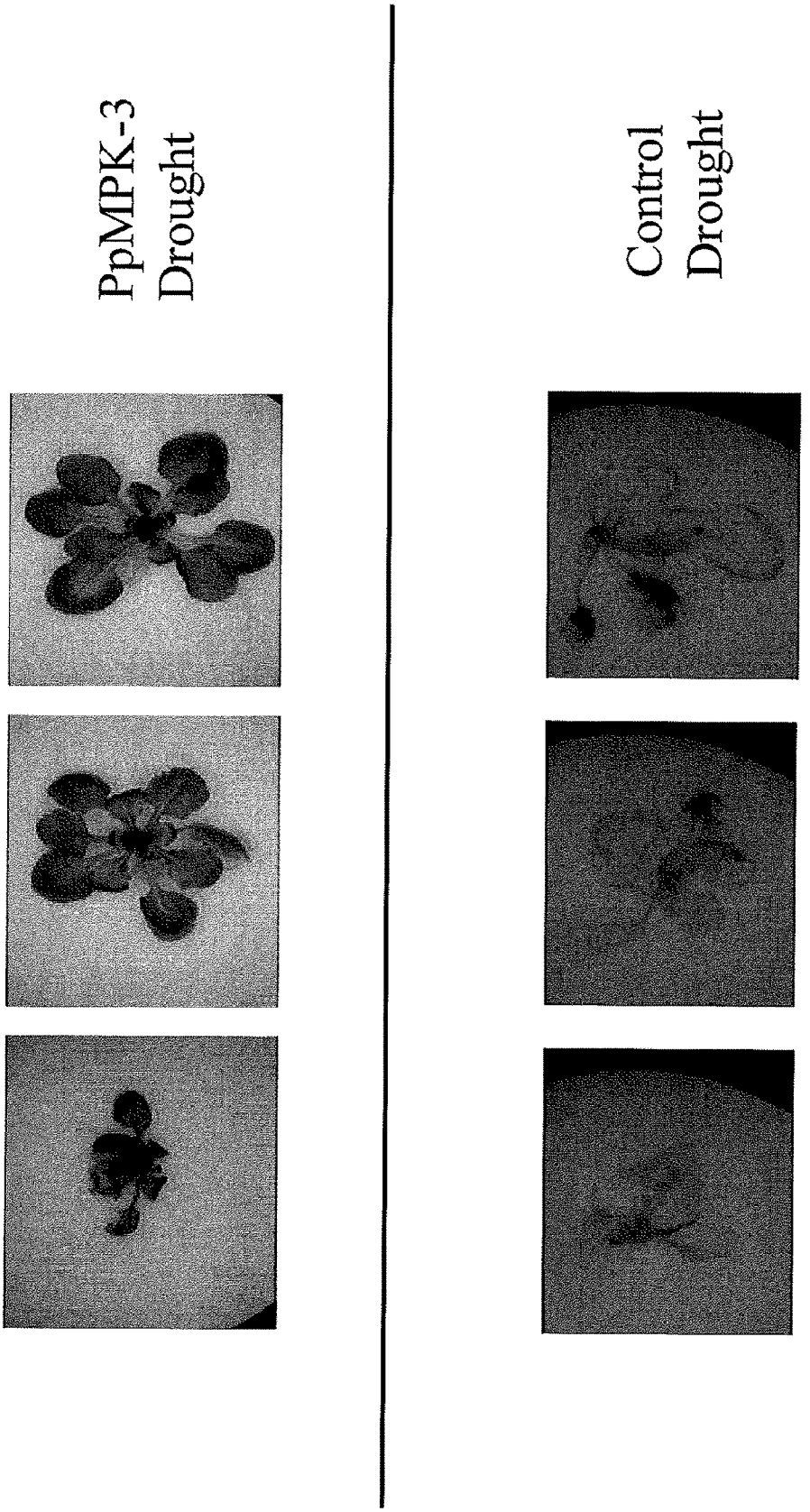


Figure 5

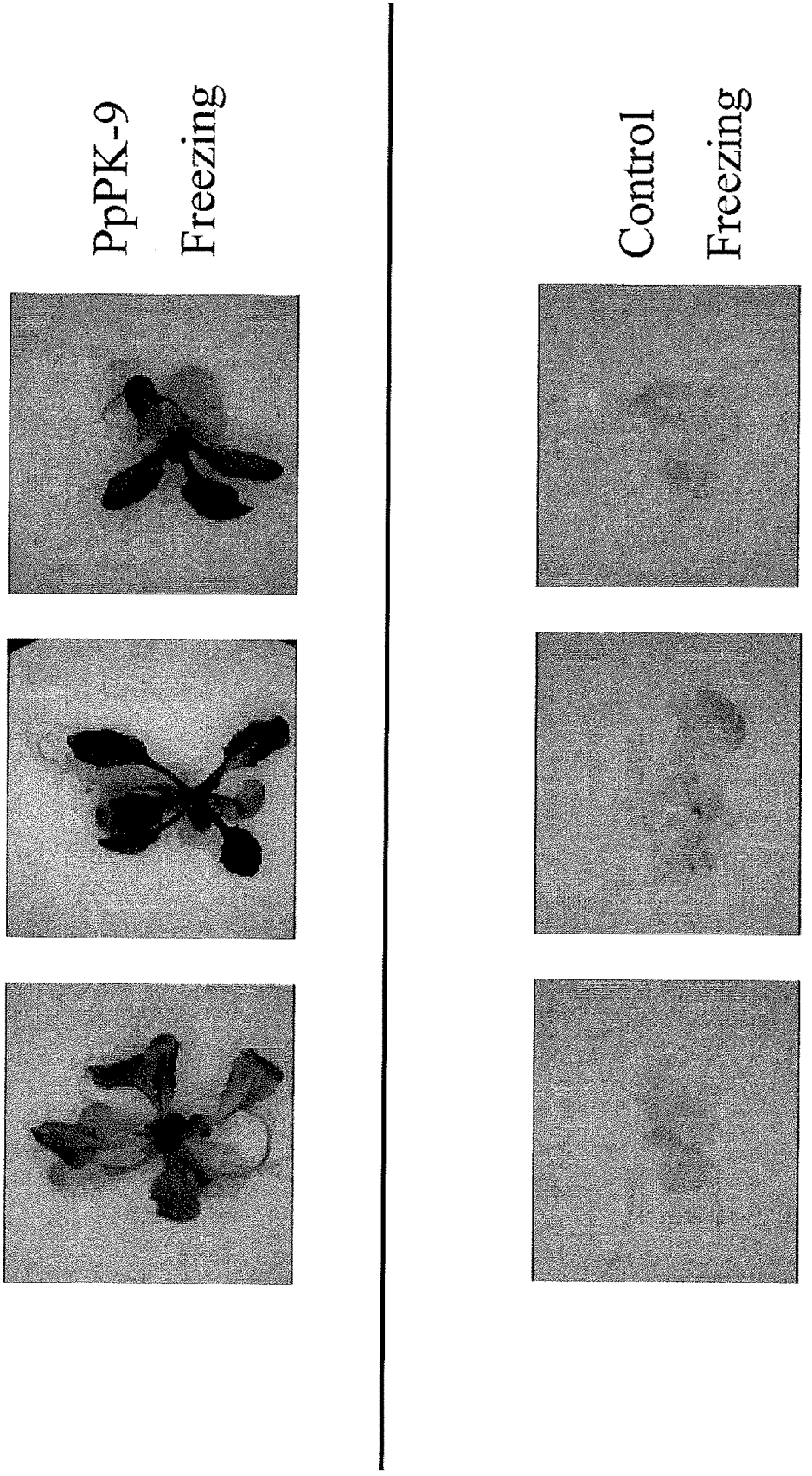


Figure 6

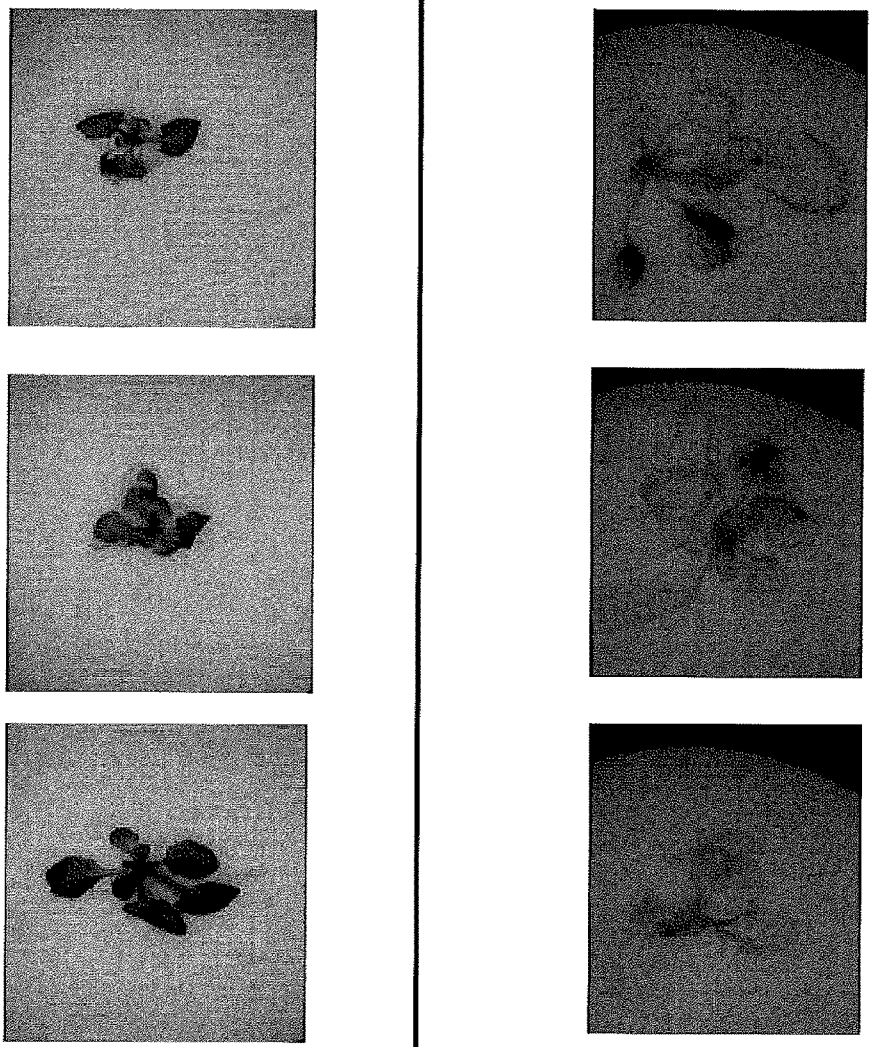
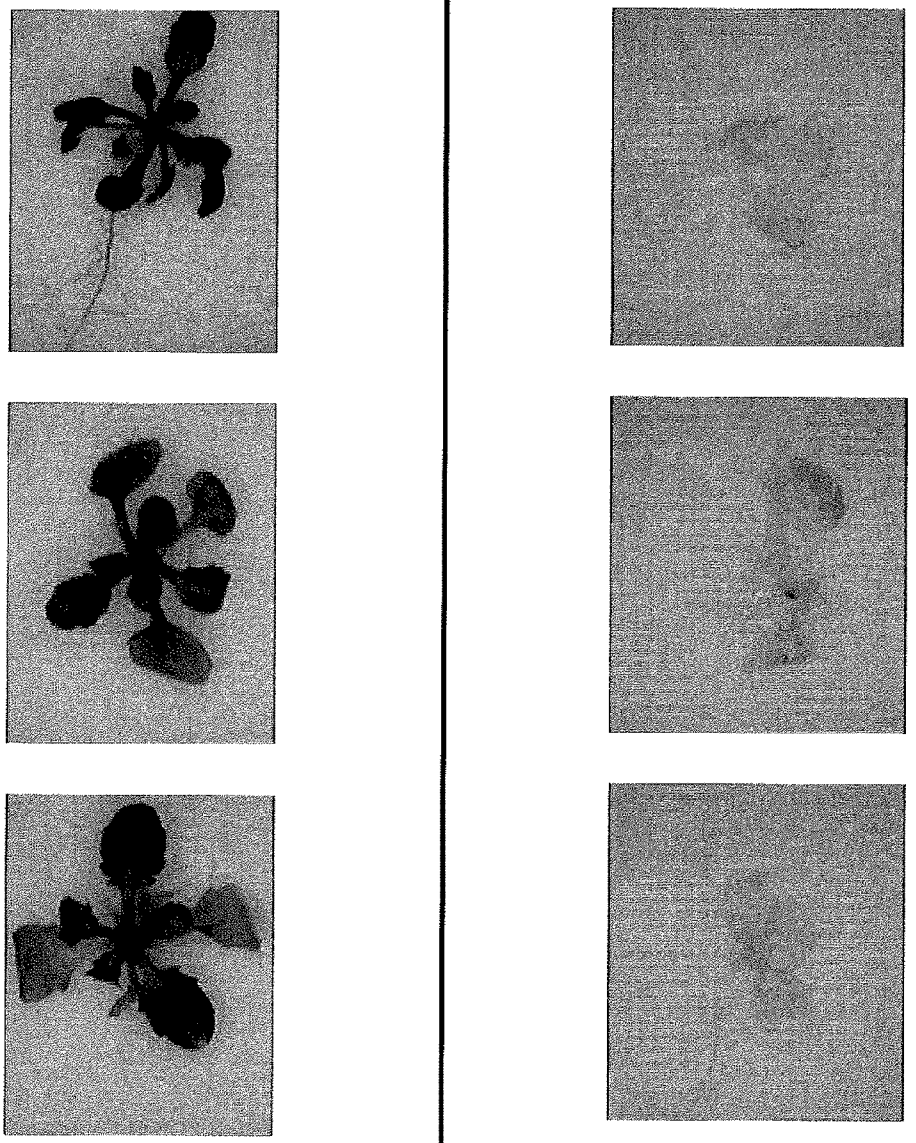


Figure 7

Figure 8



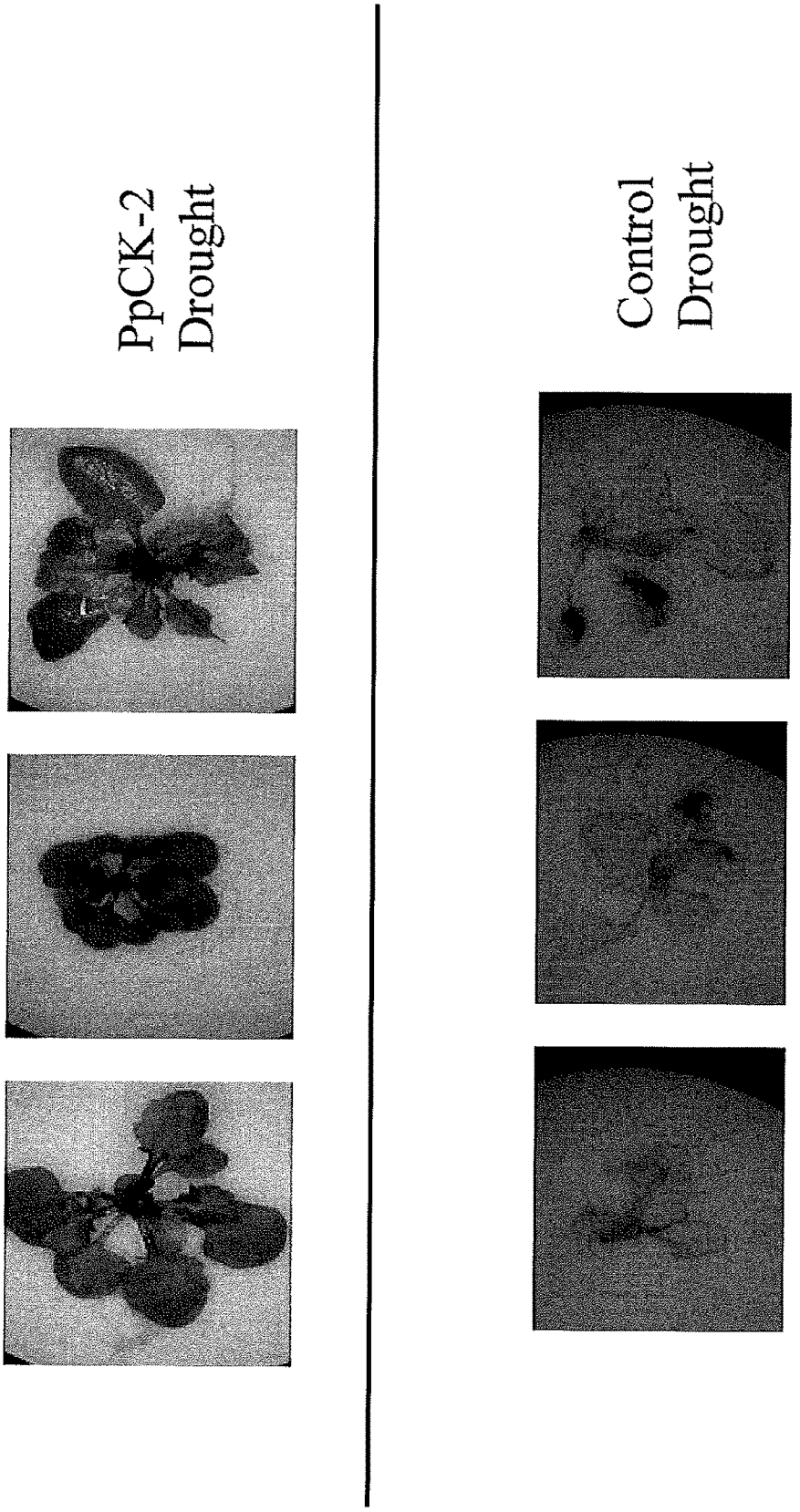


Figure 9

Figure 10

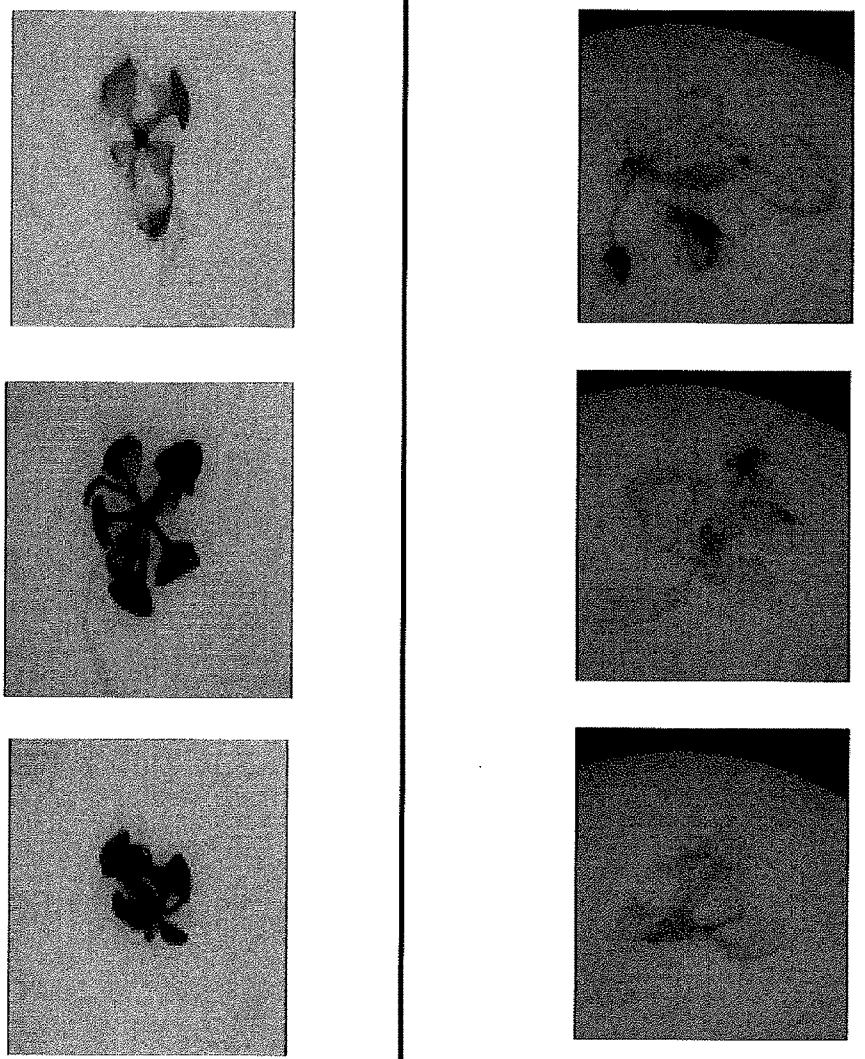


Figure 11

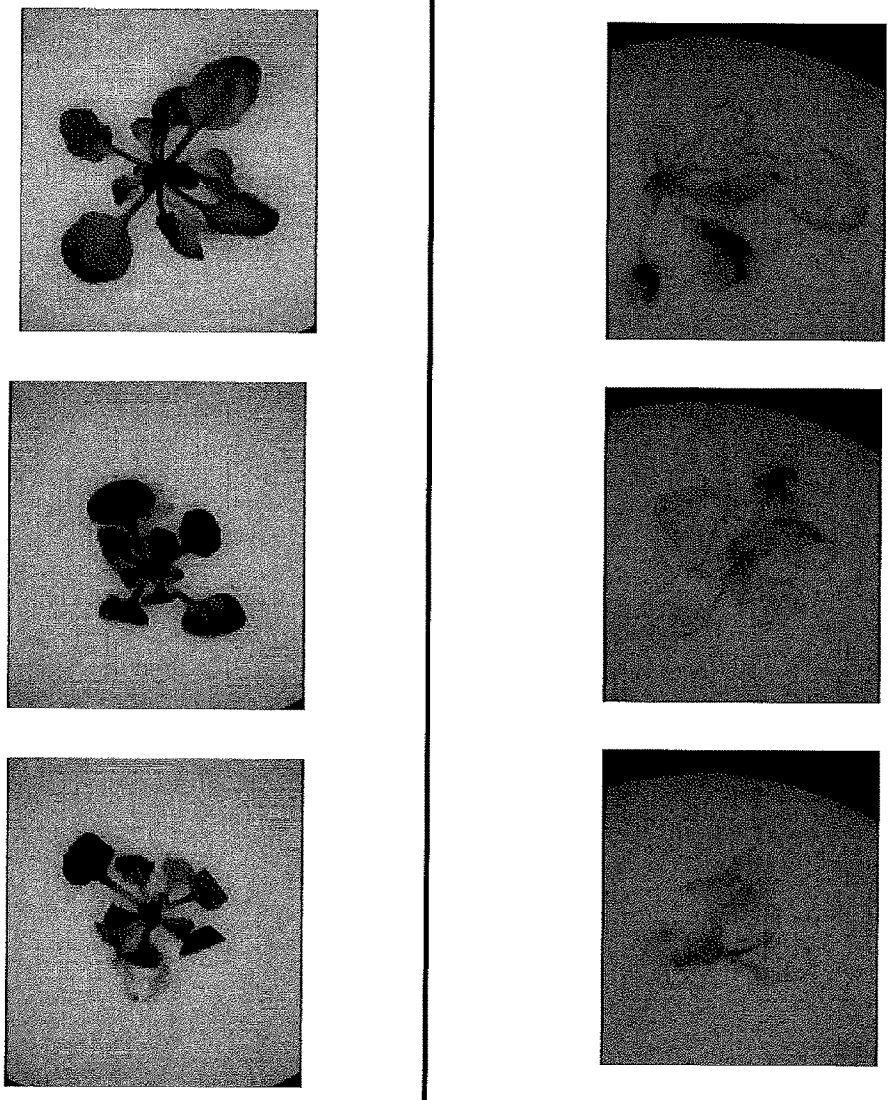


Figure 12

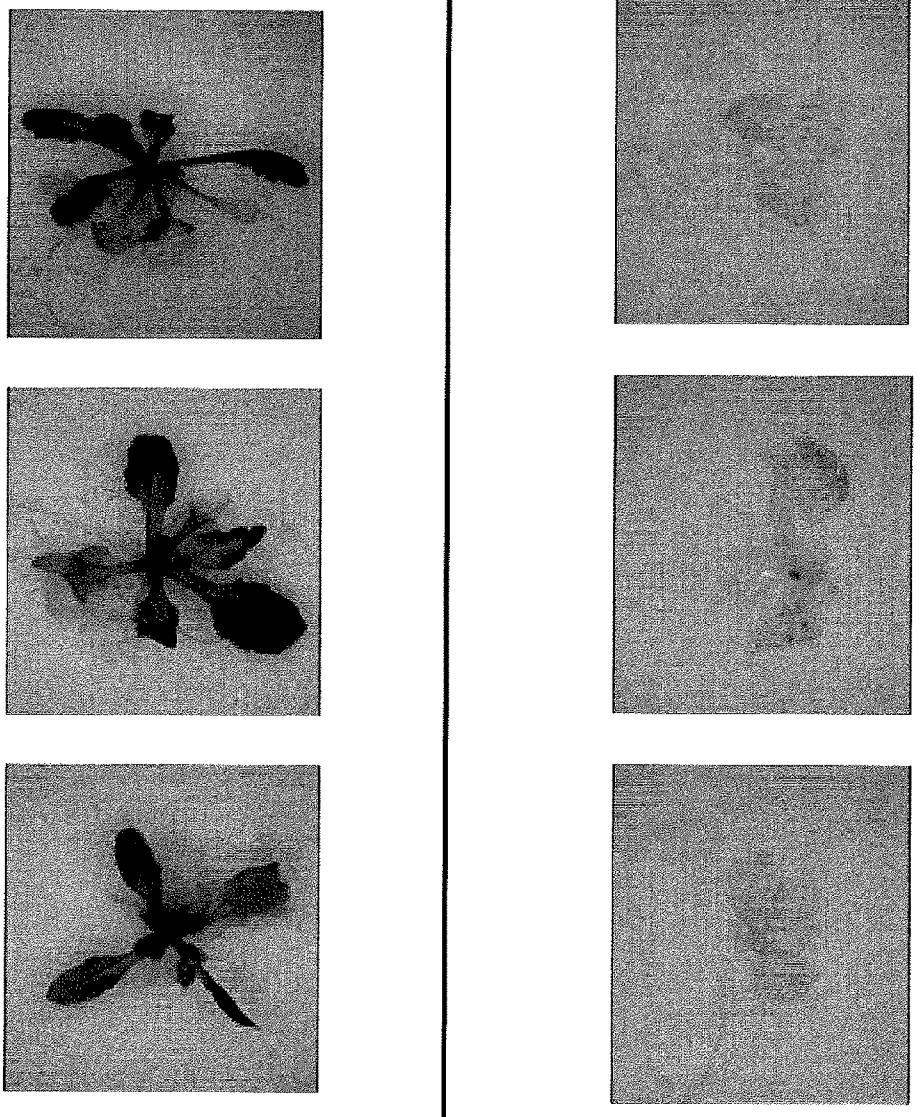


Figure 13

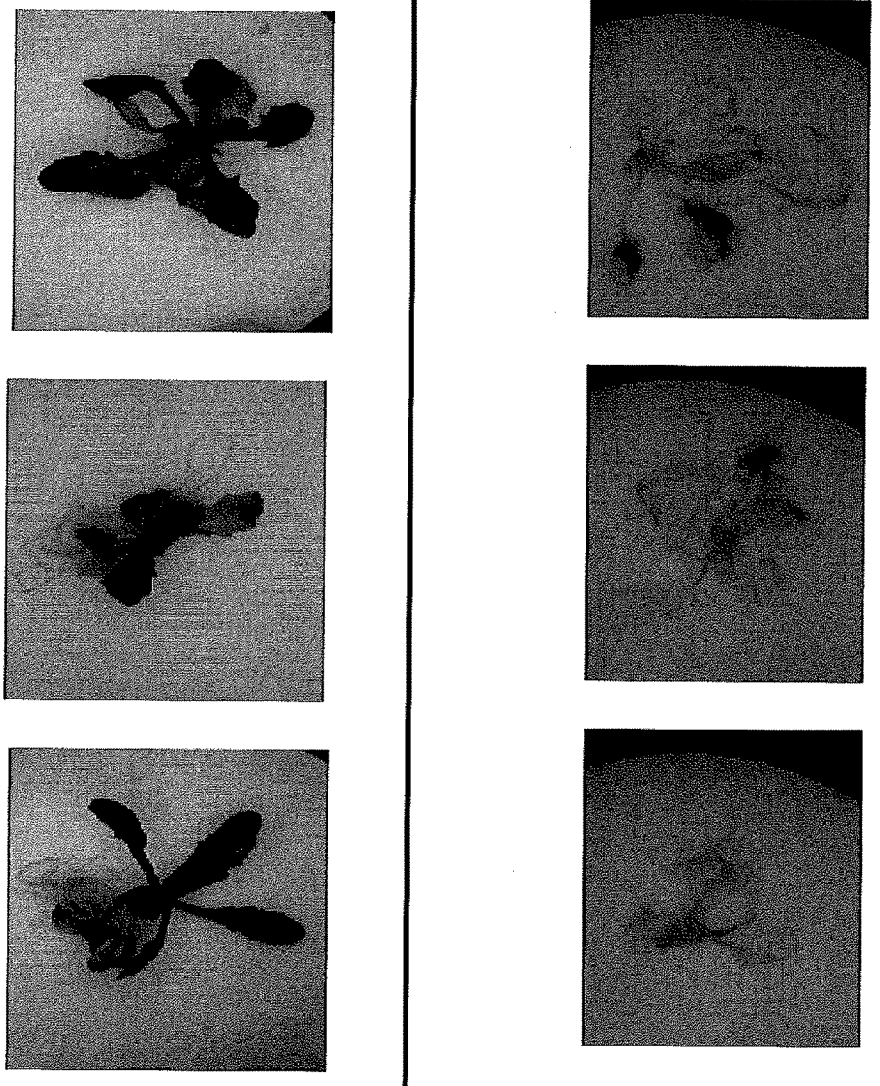


Figure 14

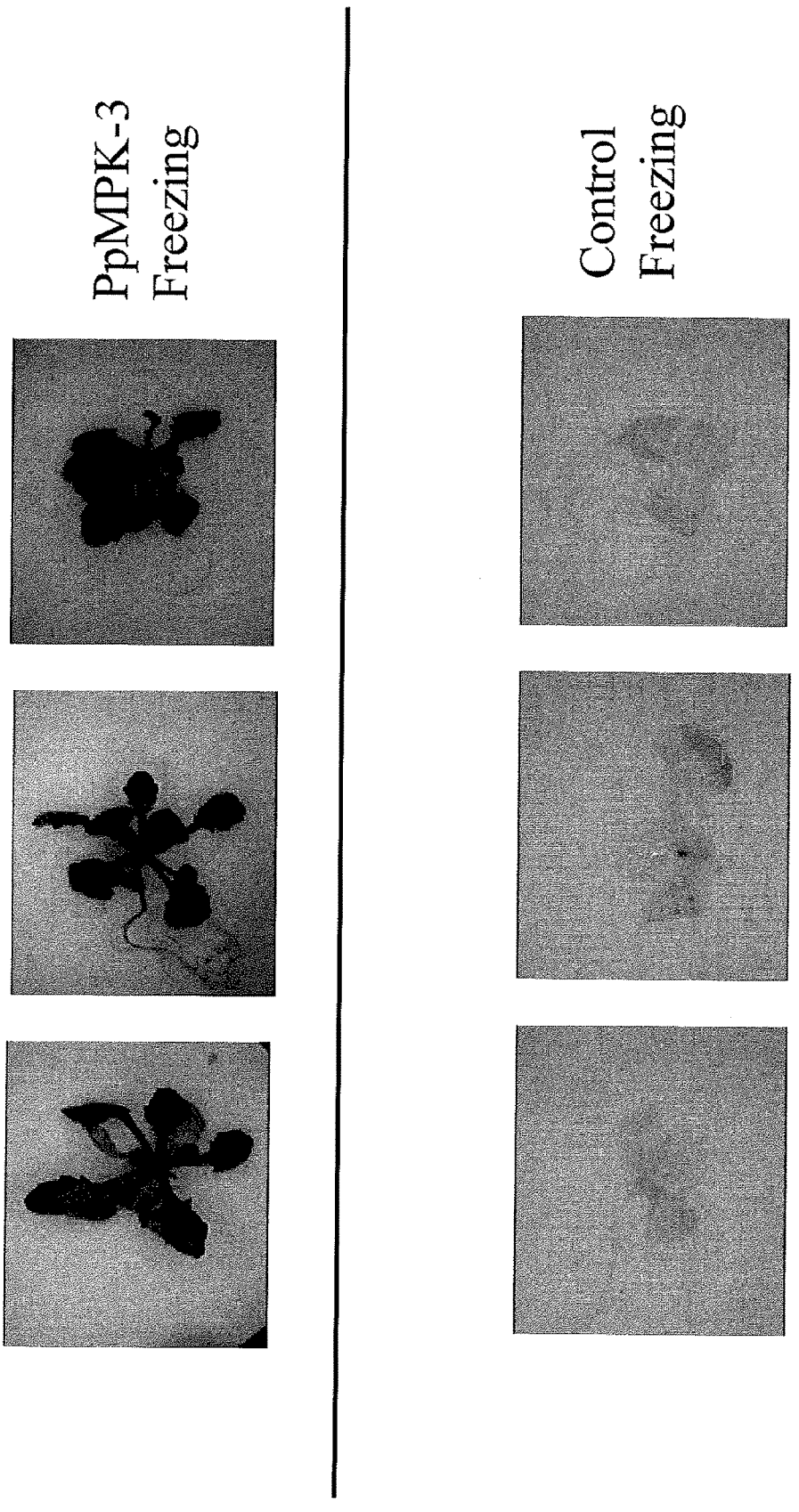
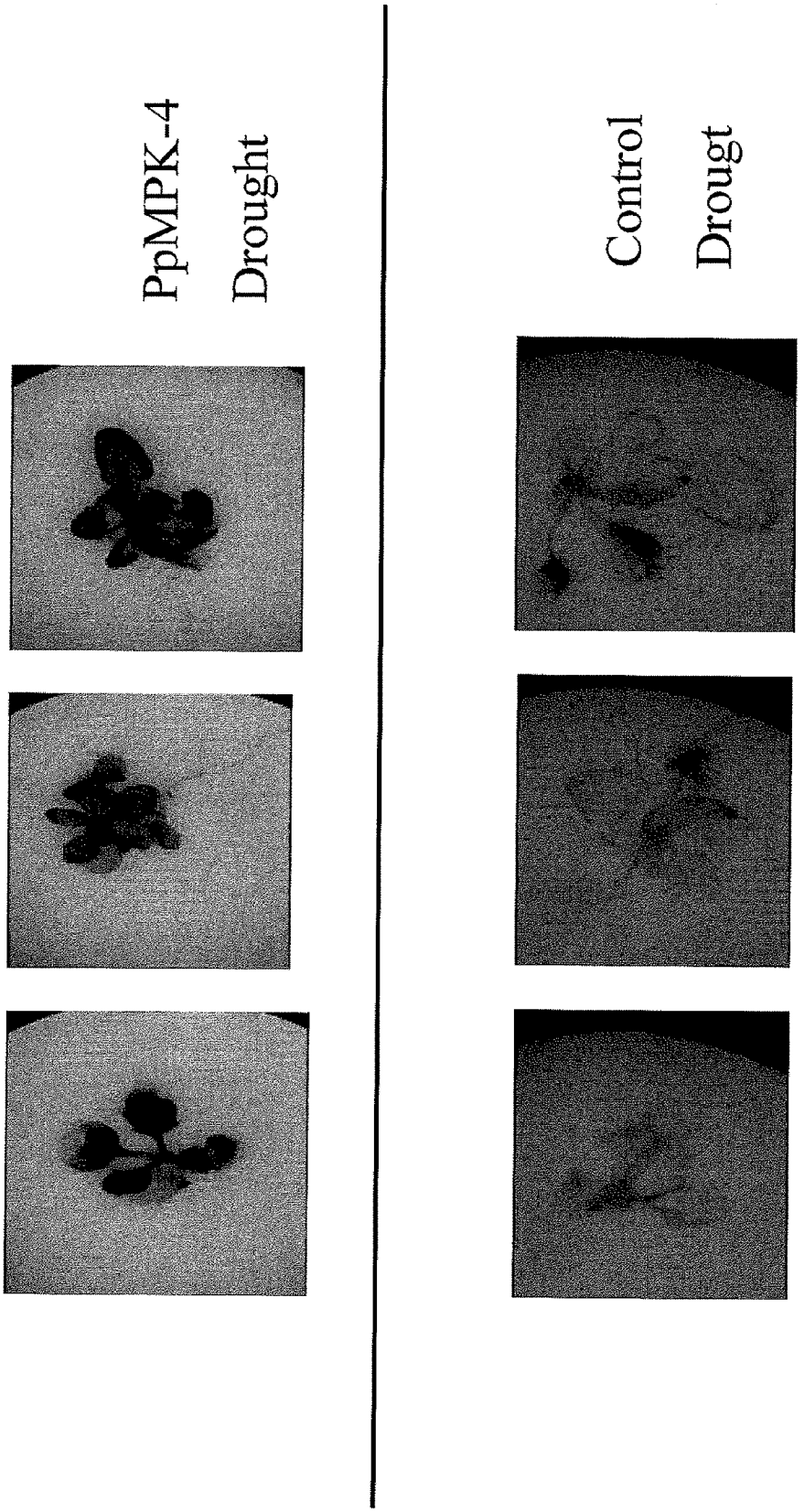


Figure 15



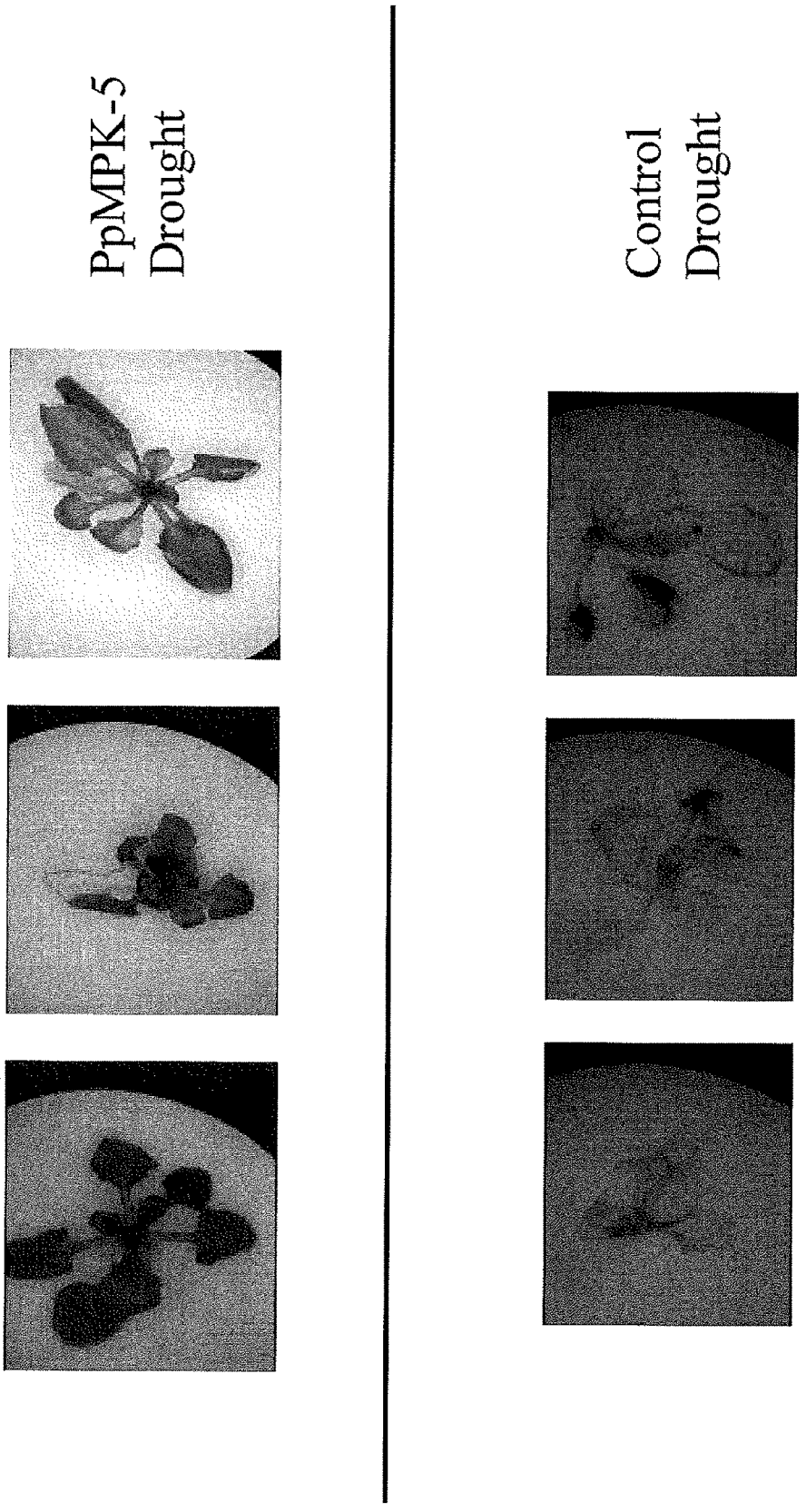


Figure 16

Figure 17

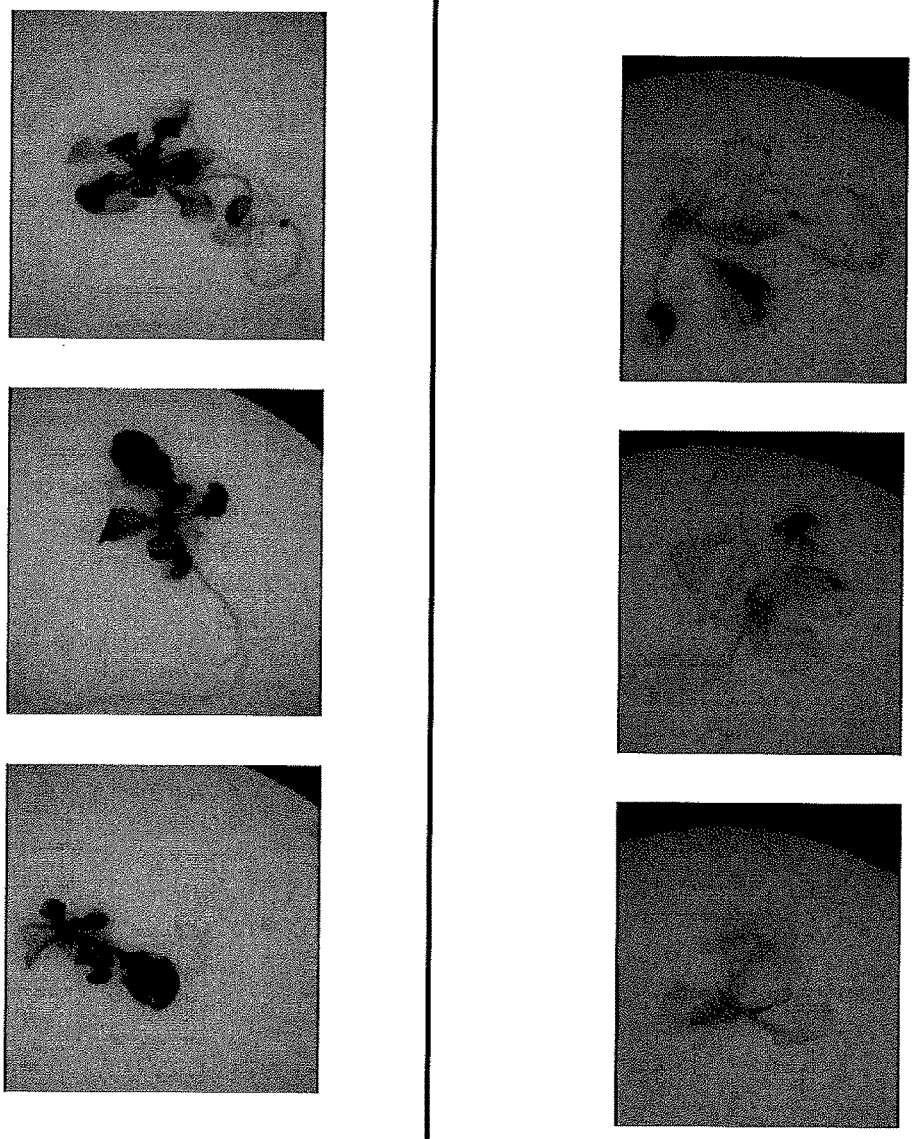
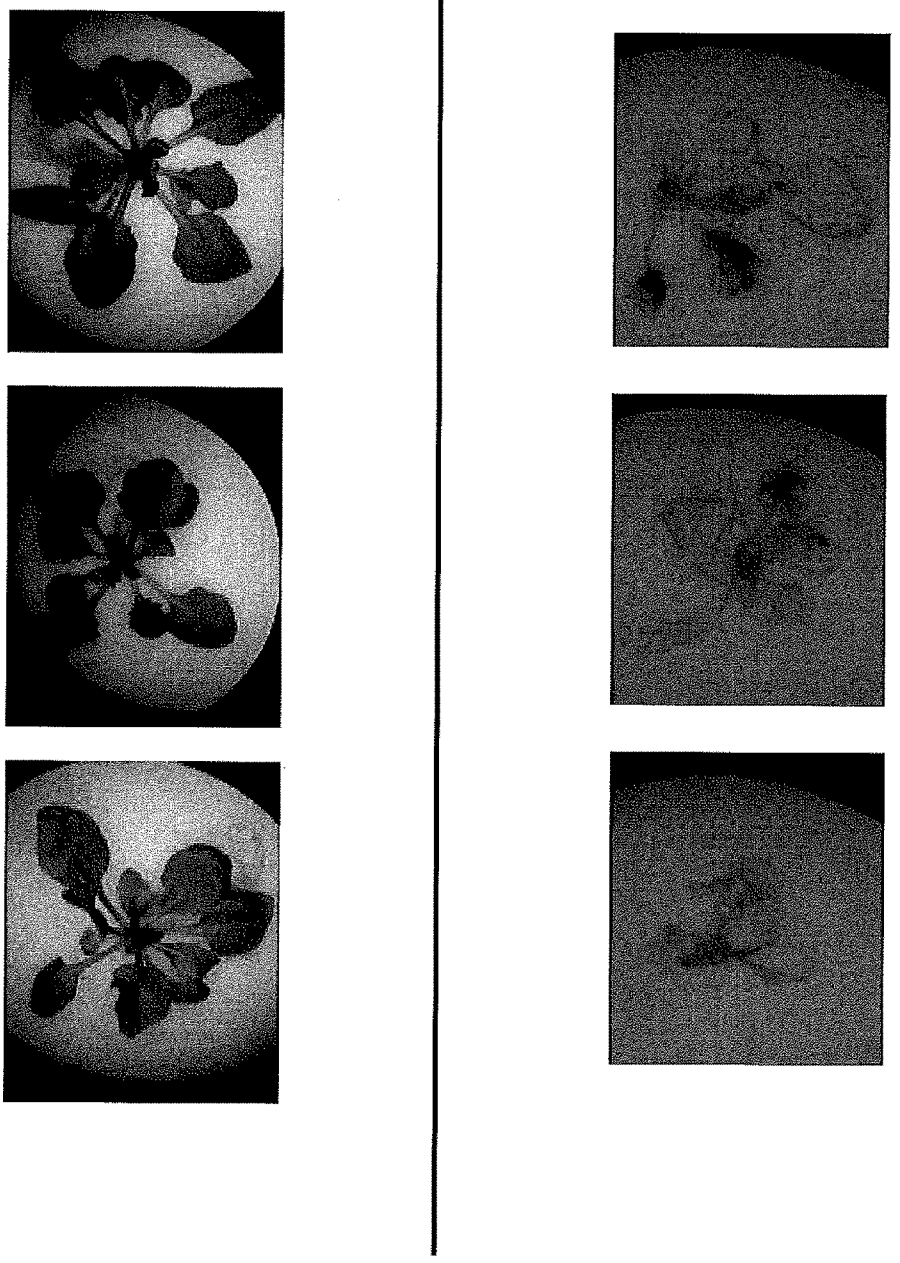


Figure 18



PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF USE IN PLANTS

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a divisional of U.S. patent application Ser. No. 09/828,313, filed Apr. 6, 2001 and now U.S. Pat. No. 6,867,351, and is with U.S. patent application Ser. No. 12/545,903, filed Aug. 24, 2009, and is with U.S. patent application Ser. No. 12/401,635, filed Mar. 11, 2009, which is with U.S. patent application Ser. No. 11/807,408, filed May 29, 2007, and now U.S. Pat. No. 7,521,597, which is with U.S. patent application Ser. No. 11/961,634, filed Dec. 20, 2007, and now U.S. Pat. No. 7,521,598, which is a continuation of U.S. patent application Ser. No. 11/564,902, filed Nov. 30, 2006, and now U.S. Pat. No. 7,504,559, which is a continuation of U.S. patent application Ser. No. 10/768,863, filed Jan. 30, 2004 and now U.S. Pat. No. 7,179,962, which is a divisional of U.S. patent application Ser. No. 09/828,313, which claims the priority benefit of U.S. Provisional Application Ser. No. 60/196,001 filed Apr. 7, 2000. The contents of each of the above-identified applications are hereby incorporated by reference.

BACKGROUND OF THE INVENTION

1. Field of the Invention

This invention relates generally to nucleic acid sequences encoding proteins that are associated with abiotic stress responses and abiotic stress tolerance in plants. In particular, this invention relates to nucleic acid sequences encoding proteins that confer drought, cold, and/or salt tolerance to plants.

2. Background Art

Abiotic environmental stresses, such as drought stress, salinity stress, heat stress, and cold stress, are major limiting factors of plant growth and productivity. Crop losses and crop yield losses of major crops such as rice, maize (corn) and wheat caused by these stresses represent a significant economic and political factor and contribute to food shortages in many underdeveloped countries.

Plants are typically exposed during their life cycle to conditions of reduced environmental water content. Most plants have evolved strategies to protect themselves against these conditions of desiccation. However, if the severity and duration of the drought conditions are too great, the effects on plant development, growth and yield of most crop plants are profound. Furthermore, most of the crop plants are very susceptible to higher salt concentrations in the soil. Continuous exposure to drought and high salt causes major alterations in the plant metabolism. These great changes in metabolism ultimately lead to cell death and consequently yield losses.

Developing stress-tolerant plants is a strategy that has the potential to solve or mediate at least some of these problems. However, traditional plant breeding strategies to develop new lines of plants that exhibit resistance (tolerance) to these types of stresses are relatively slow and require specific resistant lines for crossing with the desired line. Limited germplasm resources for stress tolerance and incompatibility in crosses between distantly related plant species represent significant problems encountered in conventional breeding. Additionally, the cellular processes leading to drought, cold and salt tolerance in model, drought- and/or salt-tolerant plants are complex in nature and involve multiple mechanisms of cellular adaptation and numerous metabolic pathways. This multi-component nature of stress tolerance has not only made breeding for tolerance largely unsuccessful, but has also limited the ability to genetically engineer stress tolerance plants using biotechnological methods.

Drought, cold as well as salt stresses have a common theme important for plant growth and that is water availability. Plants are exposed during their entire life cycle to conditions of reduced environmental water content. Most plants have evolved strategies to protect themselves against these conditions of desiccation. However, if the severity and duration of the drought conditions are too great, the effects on plant development, growth and yield of most crop plants are profound. Since high salt content in some soils result in less available water for cell intake, its effect is similar to those observed under drought conditions. Additionally, under freezing temperatures, plant cells loose water as a result of ice formation that starts in the apoplast and withdraws water from the symplast. Commonly, a plant's molecular response mechanisms to each of these stress conditions are common and protein kinases play an essential role in these molecular mechanisms.

Protein kinases represent a super family and the members of this family catalyze the reversible transfer of a phosphate group of ATP to serine, threonine and tyrosine amino acid side chains on target proteins. Protein kinases are primary elements in signaling processes in plants and have been reported to play crucial roles in perception and transduction of signals that allow a cell (and the plant) to respond to environmental stimuli. In particular, receptor protein kinases (RPKs) represent one group of protein kinases that activate a complex array of intracellular signaling pathways in response to the extracellular environment (Van der Gear et al., 1994 Annu. Rev. Cell Biol. 10:251-337). RPKs are single-pass transmembrane proteins that contain an amino-terminal signal sequence, extracellular domains unique to each receptor, and a cytoplasmic kinase domain. Ligand binding induces homo- or hetero-dimerization of RPKs, and the resultant close proximity of the cytoplasmic domains results in kinase activation by transphosphorylation. Although plants have many proteins similar to RPKs, no ligand has been identified for these receptor-like kinases (RLKs). The majority of plant RLKs that have been identified belong to the family of Serine/Threonine (Ser/Thr) kinases, and most have extracellular Leucine-rich repeats (Becraft, P W. 1998 Trends Plant Sci. 3:384-388).

Another type of protein kinase is the Ca+-dependent protein kinase (CDPK). This type of kinase has a calmodulin-like domain at the COOH terminus which allows response to Ca+ signals directly without calmodulin being present. Currently, CDPKs are the most prevalent Ser/Thr protein kinases found in higher plants. Although their physiological roles remain unclear, they are induced by cold, drought and abscisic acid (ABA) (Knight et al., 1991 Nature 352:524; Schroeder, J I and Thuleau, P., 1991 Plant Cell 3:555; Bush, D. S., 1995 Annu. Rev. Plant Phys. Plant Mol. Biol. 46:95; Urao, T. et al., 1994 Mol. Gen. Genet. 244:331).

Another type of signaling mechanism involves members of the conserved SNF1 Serine/Threonine protein kinase family. These kinases play essential roles in eukaryotic glucose and stress signaling. Plant SNF1-like kinases participate in the control of key metabolic enzymes, including HMGR, nitrate reductase, sucrose synthase, and sucrose phosphate synthase (SPS). Genetic and biochemical data indicate that sugar-dependent regulation of SNF1 kinases involves several other sensory and signaling components in yeast, plants and animals.

Additionally, members of the Mitogen-Activated Protein Kinase (MAPK) family have been implicated in the actions of

numerous environmental stresses in animals, yeasts and plants. It has been demonstrated that both MAPK-like kinase activity and mRNA levels of the components of MAPK cascades increase in response to environmental stress and plant hormone signal transduction. MAP kinases are components of sequential kinase cascades, which are activated by phosphorylation of threonine and tyrosine residues by intermediate upstream MAP kinase kinases (MAPKKs). The MAPKKs are themselves activated by phosphorylation of serine and threonine residues by upstream kinases (MAPKKKs). A number of MAP Kinase genes have been reported in higher plants.

SUMMARY OF THE INVENTION

This invention fulfills in part the need to identify new, unique protein kinases capable of conferring stress tolerance to plants upon over-expression. The present invention provides a transgenic plant cell transformed by a Protein Kinase Stress-Related Protein (PKSRP) coding nucleic acid, wherein expression of the nucleic acid sequence in the plant cell results in increased tolerance to environmental stress as compared to a wild type variety of the plant cell. Namely, described herein are the protein kinases: 1) Ser/Thr Kinase and other type of kinases (PK-6, PK-7, PK-8 and PK-9); 2) Calcium dependent protein kinases (CDPK-1 and CDPK-2), 3) Casein Kinase homologs (CK-1, CK-2 and CK-3), and 4) MAP-Kinases (MPK-2, MPK-3, MPK-4 and MPK-5), all from *Physcomitrella patens.*

The invention provides in some embodiments that the PKSRP and coding nucleic acid are that found in members of the genus *Physcomitrella.* In another preferred embodiment, the nucleic acid and protein are from a *Physcomitrella patens*. The invention provides that the environmental stress can be salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or combinations thereof. In preferred embodiments, the environmental stress can be drought or cold temperature.

The invention further provides a seed produced by a transgenic plant transformed by a PKSRP coding nucleic acid, wherein the plant is true breeding for increased tolerance to environmental stress as compared to a wild type variety of the plant. The invention further provides a seed produced by a transgenic plant expressing a PKSRP, wherein the plant is true breeding for increased tolerance to environmental stress as compared to a wild type variety of the plant.

The invention further provides an agricultural product produced by any of the below-described transgenic plants, plant parts or seeds. The invention further provides an isolated PKSRP as described below. The invention further provides an isolated PKSRP coding nucleic acid, wherein the PKSRP coding nucleic acid codes for a PKSRP as described below.

The invention further provides an isolated recombinant expression vector comprising a PKSRP coding nucleic acid as described below, wherein expression of the vector in a host cell results in increased tolerance to environmental stress as compared to a wild type variety of the host cell. The invention further provides a host cell containing the vector and a plant containing the host cell.

The invention further provides a method of producing a transgenic plant with a PKSRP coding nucleic acid, wherein expression of the nucleic acid in the plant results in increased tolerance to environmental stress as compared to a wild type variety of the plant comprising: (a) transforming a plant cell with an expression vector comprising a PKSRP coding nucleic acid, and (b) generating from the plant cell a transgenic plant with an increased tolerance to environmental stress as compared to a wild type variety of the plant. In preferred embodiments, the PKSRP and PKSRP coding nucleic acid are as described below.

The present invention further provides a method of identifying a novel PKSRP, comprising (a) raising a specific antibody response to a PKSRP, or fragment thereof, as described below; (b) screening putative PKSRP material with the antibody, wherein specific binding of the antibody to the material indicates the presence of a potentially novel PKSRP; and (c) identifying from the bound material a novel PKSRP in comparison to known PKSRP. Alternatively, hybridization with nucleic acid probes as described below can be used to identify novel PKSRP nucleic acids.

The present invention also provides methods of modifying stress tolerance of a plant comprising, modifying the expression of a PKSRP nucleic acid in the plant, wherein the PKSRP is as described below. The invention provides that this method can be performed such that the stress tolerance is either increased or decreased. Preferably, stress tolerance is increased in a plant via increasing expression of a PKSRP nucleic acid.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** shows a diagram of the plant expression vector pBPSSC022 containing the super promoter driving the expression of SEQ ID NOs: 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 and 26 ("Desired Gene"). The components are: NPTII kanamycin resistance gene (Bevan M, Nucleic Acids Res. 26: 8711-21, 1984), AtAct2-i promoter (An Y Q et al., Plant J 10: 107-121 1996), OCS3 terminator (During K, Transgenic Res. 3: 138-140, 1994), NOSpA terminator (Jefferson et al., EMBO J 6:3901-7 1987).

FIG. **2** shows the results of a drought stress test with over-expressing PpPK-6 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **3** shows the results of a drought stress test with over-expressing PpPK-7 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **4** shows the results of a freezing stress test with over-expressing PpPK-7 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **5** shows the results of a drought stress test with over-expressing PpPK-9 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **6** shows the results of a freezing stress test with over-expressing PpPK-9 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **7** shows the results of a drought stress test with over-expressing PpCK-1 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **8** shows the results of a freezing stress test with over-expressing PpCK-1 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **9** shows the results of a drought stress test with over-expressing PpCK-2 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **10** shows the results of a drought stress test with over-expressing PpCK-3 transgenic plants and wild-type

Arabidopsis lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **11** shows the results of a drought stress test with over-expressing PpMPK-2 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **12** shows the results of a freezing stress test with over-expressing PpMPK-2 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **13** shows the results of a drought stress test with over-expressing PpMPK-3 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **14** shows the results of a freezing stress test with over-expressing PpMPK-3 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **15** shows the results of a drought stress test with over-expressing PpMPK-4 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **16** shows the results of a drought stress test with over-expressing PpMPK-5 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **17** shows the results of a drought stress test with over-expressing PpCPK-1 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

FIG. **18** shows the results of a drought stress test with over-expressing PpCPK-2 transgenic plants and wild-type *Arabidopsis* lines. The transgenic lines display a tolerant phenotype. Individual transformant lines are shown.

DETAILED DESCRIPTION OF THE INVENTION

The present invention may be understood more readily by reference to the following detailed description of the preferred embodiments of the invention and the Examples included herein. However, before the present compounds, compositions, and methods are disclosed and described, it is to be understood that this invention is not limited to specific nucleic acids, specific polypeptides, specific cell types, specific host cells, specific conditions, or specific methods, etc., as such may, of course, vary, and the numerous modifications and variations therein will be apparent to those skilled in the art. It is also to be understood that the terminology used herein is for the purpose of describing specific embodiments only and is not intended to be limiting. In particular, the designation of the amino acid sequences as protein "Protein Kinase Stress-Related Proteins" (PKSRPs), in no way limits the functionality of those sequences.

The present invention provides a transgenic plant cell transformed by a PKSRP coding nucleic acid, wherein expression of the nucleic acid sequence in the plant cell results in increased tolerance to environmental stress as compared to a wild type variety of the plant cell. The invention further provides transgenic plant pails and transgenic plants containing the plant cells described herein. Also provided is a plant seed produced by a transgenic plant transformed by a PKSRP coding nucleic acid, wherein the seed contains the PKSRP coding nucleic acid, and wherein the plant is true breeding for increased tolerance to environmental stress as compared to a wild type variety of the plant. The invention further provides a seed produced by a transgenic plant expressing a PKSRP, wherein the seed contains the PKSRP, and wherein the plant is true breeding for increased tolerance to environmental stress as compared to a wild type variety of the plant. The invention also provides an agricultural product produced by any of the below-described transgenic plants, plant parts and plant seeds.

As used herein, the term "variety" refers to a group of plants within a species that share constant characters that separate them from the typical form and from other possible varieties within that species. While possessing at least one distinctive trait, a variety is also characterized by some variation between individuals within the variety, based primarily on the Mendelian segregation of traits among the progeny of succeeding generations. A variety is considered "true breeding" for a particular trait if it is genetically homozygous for that trait to the extent that when the true-breeding variety is self-pollinated, a significant amount of independent segregation of the trait among the progeny is not observed. In the present invention, the trait arises from the transgenic expression of one or more DNA sequences introduced into a plant variety.

The present invention describes for the first time that the *Physcomitrella patens* PKSRPs, PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2, are useful for increasing a plant's tolerance to environmental stress. Accordingly, the present invention provides isolated PKSRPs selected from the group consisting of PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2, and homologs thereof. In preferred embodiments, the PKSRP is selected from 1) Protein Kinase-6 (PK-6) protein as defined in SEQ ID NO:27; 2) Protein Kinase-7 (PK-7) protein as defined in SEQ ID NO:28; 3) Protein Kinase-8 (PK-8) protein as defined in SEQ ID NO:29; 4) Protein Kinase-9 (PK-9) protein as defined in SEQ ID NO:30; 5) Casein Kinase homologue (CK-1) protein as defined in SEQ ID NO:31; 6) Casein Kinase homologue-2 (CK-2) protein as defined in SEQ ID NO:32; 7) Casein Kinase homologue-3 (CK-3) protein as defined in SEQ ID NO:33; 8) MAP Kinase-2 (MPK-2) protein as defined in SEQ ID NO:34; 9) MAP Kinase-3 (MPK-3) protein as defined in SEQ ID NO:35; 10) MAP Kinase-4 (MPK-4) protein as defined in SEQ ID NO:36; 11) MAP Kinase-5 (MPK-5) protein as defined in SEQ ID NO:37, 12) Calcium dependent protein kinase-1 (CPK-1) protein as defined in SEQ ID NO:38; 13) Calcium dependent protein kinase-2 (CPK-2) protein as defined in SEQ ID NO:39; and homologs and orthologs thereof Homologs and orthologs of the amino acid sequences are defined below.

The PKSRPs of the present invention are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described below), the expression vector is introduced into a host cell (as described below) and the PKSRP is expressed in the host cell. The PKSRP can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, a PKSRP polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native PKSRP can be isolated from cells (e.g., *Physcomitrella patens*), for example using an anti-PKSRP antibody, which can be produced by standard techniques utilizing a PKSRP or fragment thereof.

The invention further provides an isolated PKSRP coding nucleic acid. The present invention includes PKSRP coding nucleic acids that encode PKSRPs as described herein. In preferred embodiments, the PKSRP coding nucleic acid is selected from 1) Protein Kinase-6 (PK-6) nucleic acid as defined in SEQ ID NO:14; 2) Protein Kinase-7 (PK-7)

nucleic acid as defined in SEQ ID NO:15; 3) Protein Kinase-8 (PK-8) nucleic acid as defined in SEQ ID NO:16; 4) Protein Kinase-9 (PK-9) nucleic acid as defined in SEQ ID NO:17; 5) Casein Kinase homolog (CK-1) nucleic acid as defined in SEQ ID NO:18; 6) Casein Kinase homolog-2 (CK-2) nucleic acid as defined in SEQ ID NO:19; 7) Casein Kinase homolog-3 (CK-3) nucleic acid as defined in SEQ ID NO:20; 8) MAP Kinase-2 (MPK-2) nucleic acid as defined in SEQ ID NO:21; 9) MAP Kinase-3 (MPK-3) nucleic acid as defined in SEQ ID NO:22; 10) MAP Kinase-4 (MPK-4) nucleic acid as defined in SEQ ID NO:23; 11) MAP Kinase-5 (MPK-5) nucleic acid as defined in SEQ ID NO:24; 12) Calcium dependent protein kinase-1 (CPK-1) nucleic acid as defined in SEQ ID NO:25; 13) Calcium dependent protein kinase-2 (CPK-2) nucleic acid as defined in SEQ ID NO:26 and homologs and orthologs thereof Homologs and orthologs of the nucleotide sequences are defined below. In one preferred embodiment, the nucleic acid and protein are isolated from the plant genus *Physcomitrella*. In another preferred embodiment, the nucleic acid and protein are from a *Physcomitrella patens* (*P. patens*) plant.

As used herein, the term "environmental stress" refers to any sub-optimal growing condition and includes, but is not limited to, sub-optimal conditions associated with salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or combinations thereof In preferred embodiments, the environmental stress can be salinity, drought, or temperature, or combinations thereof, and in particular, can be high salinity, low water content or low temperature. It is also to be understood that as used in the specification and in the claims, "a" or "an" can mean one or more, depending upon the context in which it is used. Thus, for example, reference to "a cell" can mean that at least one cell can be utilized.

As also used herein, the terms "nucleic acid" and "nucleic acid molecule" are intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 1000 nucleotides of sequence upstream from the 5' end of the coding region and at least about 200 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one that is substantially separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of some of the sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated PKSRP nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g., a *Physcomitrella patens* cell). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be free from some of the other cellular material with which it is naturally associated, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having a nucleotide sequence of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ 1D NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *P. patens* PKSRP cDNA can be isolated from a *P. patens* library using all or portion of one of the sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID N0:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12 and SEQ ID NO:13. Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12 and SEQ ID NO:13 can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence. For example, mRNA can be isolated from plant cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin et al., 1979 Biochemistry 18:5294-5299) and cDNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, Md.; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, Fla.). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12 and SEQ ID NO:13. A nucleic acid molecule of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid molecule so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to a PKSRP nucleotide sequence can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26. These cDNAs comprise sequences encoding the PKSRPs (i.e., the "coding region", indicated in Table 1), as well as 5' untranslated sequences and 3' untranslated sequences. It is to be understood that SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26 comprise both coding regions and 5' and 3' untranslated regions. Alternatively, the nucleic acid molecules of the present invention can comprise only the coding region of any of the sequences in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26 or can contain whole genomic fragments isolated from genomic DNA. A coding region of these sequences is indicated as "ORF position". The present invention also includes PKSRP coding nucleic acids that encode PKSRPs as described herein. Preferred is a PKSRP coding nucleic acid that encodes a PKSRP selected from the group consisting of, PK-6 (SEQ ID NO:27), PK-7 (SEQ ID NO:28), PK-8 (SEQ ID NO:29), PK-9 (SEQ ID NO:30), CK-1 (SEQ ID NO:31), CK-2 (SEQ

ID NO:32), CK-3 (SEQ ID NO:33), MPK-2 (SEQ ID NO:34), MPK-3 (SEQ ID NO:35), MPK-4 (SEQ ID NO:36), MPK-5 (SEQ ID NO:37), CPK-1 (SEQ ID NO:38) and CPK-2 (SEQ ID NO:39).

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26, for example, a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of a PKSRP. The nucleotide sequences determined from the cloning of the PKSRP genes from *P. patens* allow for the generation of probes and primers designed for use in identifying and/or cloning PKSRP homologs in other cell types and organisms, as well as PKSRP homologs from other mosses and related species.

Portions of proteins encoded by the PKSRP nucleic acid molecules of the invention are preferably biologically active portions of one of the PKSRPs described herein. As used herein, the term "biologically active portion of" a PKSRP is intended to include a portion, e.g., a domain/motif, of a PKSRP that participates in a stress tolerance response in a plant, has an activity as set forth in Table 1, or participates in the transcription of a protein involved in a stress tolerance response in a plant. To determine whether a PKSRP, or a biologically active portion thereof, can participate in transcription of a protein involved in a stress tolerance response in a plant, or whether repression of a PKSRP results in increased stress tolerance in a plant, a stress analysis of a plant comprising the PKSRP may be performed. Such analysis methods are well known to those skilled in the art, as detailed in Example 7. More specifically, nucleic acid fragments encoding biologically active portions of a PKSRP can be prepared by isolating a portion of one of the sequences in SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39, expressing the encoded portion of the PKSRP or peptide (e.g., by recombinant expression in vitro) and assessing the activity of the encoded portion of the PKSRP or peptide.

Biologically active portions of a PKSRP are encompassed by the present invention and include peptides comprising amino acid sequences derived from the amino acid sequence of a PKSRP, e.g., an amino acid sequence of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 or SEQ ID NO:39, or the amino acid sequence of a protein homologous to a PKSRP, which include fewer amino acids than a full length PKSRP or the full length protein which is homologous to a PKSRP, and exhibit at least one activity of a PKSRP. Typically, biologically active portions (e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of a PKSRP. Moreover, other biologically active portions in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of a PKSRP include one or more selected domains/motifs or portions thereof having biological activity.

The invention also provides PKSRP chimeric or fusion proteins. As used herein, a PKSRP "chimeric protein" or "fusion protein" comprises a PKSRP polypeptide operatively linked to a non-PKSRP polypeptide. A PKSRP polypeptide refers to a polypeptide having an amino acid sequence corresponding to a PKSRP, whereas a non-PKSRP polypeptide refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the PKSRP, e.g., a protein that is different from the PKSRP and is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the PKSRP polypeptide and the non-PKSRP polypeptide are fused to each other so that both sequences fulfill the proposed function attributed to the sequence used. The non-PKSRP polypeptide can be fused to the N-terminus or C-terminus of the PKSRP polypeptide. For example, in one embodiment, the fusion protein is a GST-PKSRP fusion protein in which the PKSRP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant PKSRPs. In another embodiment, the fusion protein is a PKSRP containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression and/or secretion of a PKSRP can be increased through use of a heterologous signal sequence.

Preferably, a PKSRP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, for example, Current Protocols in Molecular Biology, Eds. Ausubel et al. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A PKSRP encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the PKSRP.

In addition to fragments and fusion proteins of the PKSRPs described herein, the present invention includes homologs and analogs of naturally occurring PKSRPs and PKSRP encoding nucleic acids in a plant. "Homologs" are defined herein as two nucleic acids or proteins that have similar, or "homologous", nucleotide or amino acid sequences, respectively. Homologs include allelic variants, orthologs, paralogs, agonists and antagonists of PKSRPs as defined hereafter. The term "homolog" further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26 (and portions thereof) due to degeneracy of the genetic code and thus encode the same PKSRP as that encoded by the nucleotide sequences shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26. As used herein a "naturally occurring" PKSRP refers to a PKSRP amino acid sequence that occurs in nature. Prefer-

ably, a naturally occurring PKSRP comprises an amino acid sequence selected from the group consisting of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39.

An agonist of the PKSRP can retain substantially the same, or a subset, of the biological activities of the PKSRP. An antagonist of the PKSRP can inhibit one or more of the activities of the naturally occurring form of the PKSRP. For example, the PKSRP antagonist can competitively bind to a downstream or upstream member of the cell membrane component metabolic cascade that includes the PKSRP, or bind to a PKSRP that mediates transport of compounds across such membranes, thereby preventing translocation from taking place.

Nucleic acid molecules corresponding to natural allelic variants and analogs, orthologs and paralogs of a PKSRP cDNA can be isolated based on their identity to the *Physcomitrella patens* PKSRP nucleic acids described herein using PKSRP cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. In an alternative embodiment, homologs of the PKSRP can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the PKSRP for PKSRP agonist or antagonist activity. In one embodiment, a variegated library of PKSRP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of PKSRP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential PKSRP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of PKSRP sequences therein. There are a variety of methods that can be used to produce libraries of potential PKSRP homologs from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene is then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential PKSRP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang, S. A., 1983 Tetrahedron 39:3; Itakura et al., 1984 Annu. Rev. Biochem. 53:323; Itakura et al., 1984 Science 198:1056; Ike et al., 1983 Nucleic Acid Res. 11:477).

In addition, libraries of fragments of the PKSRP coding regions can be used to generate a variegated population of PKSRP fragments for screening and subsequent selection of homologs of a PKSRP. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a PKSRP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA, which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S I nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the PKSRP.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of PKSRP homologs. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify PKSRP homologs (Arkin and Yourvan, 1992 PNAS 89:7811-7815; Delgrave et al., 1993 Protein Engineering 6(3):327-331). In another embodiment, cell based assays can be exploited to analyze a variegated PKSRP library, using methods well known in the art. The present invention further provides a method of identifying a novel PKSRP, comprising (a) raising a specific antibody response to a PKSRP, or a fragment thereof, as described herein; (b) screening putative PKSRP material with the antibody, wherein specific binding of the antibody to the material indicates the presence of a potentially novel PKSRP; and (c) analyzing the bound material in comparison to known PKSRP, to determine its novelty.

To determine the percent homology of two amino acid sequences (e.g., one of the sequences of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39 and a mutant form thereof), the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (e.g., one of the sequences of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39) is occupied by the same amino acid residue as the corresponding position in the other sequence (e.g., a mutant form of the sequence selected from the polypeptide of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39), then the molecules are homologous at that position (i.e., as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The same type of comparison can be made between two nucleic acid sequences.

The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % homology=numbers of identical positions/total numbers of positions×100). Preferably, the amino acid sequences included in the present invention are at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence shown in SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 or SEQ ID NO:39. In yet another embodiment, at least about 50-60%, preferably at least about

60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence encoded by a nucleic acid sequence shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26. In other embodiments, the preferable length of sequence comparison for proteins is at least 15 amino acid residues, more preferably at least 25 amino acid residues, and most preferably at least 35 amino acid residues.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50-60%, preferably at least about 60-70%, more preferably at least about 70-80%, 80-90%, or 90-95%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26, or a portion thereof The preferable length of sequence comparison for nucleic acids is at least 75 nucleotides, more preferably at least 100 nucleotides and most preferably the entire length of the coding region.

It is also preferable that the homologous nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 or SEQ ID NO:39 such that the protein or portion thereof maintains the same or a similar function as the amino acid sequence to which it is compared. Functions of the PKSRP amino acid sequences of the present invention include the ability to participate in a stress tolerance response in a plant, or more particularly, to participate in the transcription of a protein involved in a stress tolerance response in a *Physcomitrella patens* plant. Examples of such activities are described in Table 1.

In addition to the above described methods, a determination of the percent homology between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990 Proc. Natl. Acad. Sci. USA 90:5873-5877). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990 J. Mol. Biol. 215:403-410).

BLAST nucleic acid searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleic acid sequences homologous to the PKSRP nucleic acid molecules of the invention. Additionally, BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to PKSRPs of the present invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997 Nucleic Acids Res. 25:3389-3402). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. Another preferred non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (CABIOS 1989). Such an algorithm is incorporated into the ALIGN program (version 2.0) that is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4 can be used to obtain amino acid sequences homologous to the PKSRPs of the present invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997 Nucleic Acids Res. 25:3389-3402). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. Another preferred non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (CABIOS 1989). Such an algorithm is incorporated into the ALIGN program (version 2.0) that is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4 can be used.

Finally, homology between nucleic acid sequences can also be determined using hybridization techniques known to those of skill in the art. Accordingly, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the nucleotide sequences shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26, or a portion thereof. More particularly, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length.

As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology,* 6.3.1-6.3.6, John Wiley & Sons, N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6× sodium chloride/sodium citrate (SSC) at about 45° C., followed by one or more washes in 0.2×SSC, 0.1% SDS at 50-65° C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26 corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a naturally occurring *Physcomitrella patens* PKSRP.

Using the above-described methods, and others known to those of skill in the art, one of ordinary skill in the art can isolate homologs of the PKSRPs comprising amino acid sequences shown in SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 or SEQ ID NO:39. One subset of these homologs are allelic variants. As used herein, the term "allelic variant" refers to a nucleotide sequence containing polymorphisms that lead to changes in the amino acid sequences of a PKSRP and that exist within a natural population (e.g., a plant species or variety). Such natural allelic variations can typically result in 1-5% variance in a PKSRP nucleic acid. Allelic variants can be identified by sequencing the nucleic acid sequence of interest in a number of different plants, which can be readily carried out by using hybridization probes to identify the same PKSRP genetic locus in those plants. Any and all such nucleic acid variations and resulting amino acid polymorphisms or variations in a PKSRP that are the result of natural allelic variation and that do not alter the functional activity of a PKSRP, are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding PKSRPs from the same or other species such as PKSRP analogs, orthologs and paralogs, are intended to be within the scope of the present invention. As used herein, the term "analogs" refers to two nucleic acids that have the same or similar function, but that have evolved separately in unrelated organisms. As used herein, the term "orthologs" refers to two nucleic acids from different species, but that have evolved from a common ancestral gene by speciation. Normally, orthologs encode proteins having the same or similar functions. As also used herein, the term "paralogs" refers to two nucleic acids that are related by duplication within a genome. Paralogs usually have different functions, but these functions may be related (Tatusov, R. L. et al. 1997 Science 278(5338):631-637). Analogs, orthologs and paralogs of a naturally occurring PKSRP can differ from the naturally occurring PKSRP by post-translational modifications, by amino acid sequence differences, or by both. Post-translational modifications include in vivo and in vitro chemical derivatization of polypeptides, e.g., acetylation, carboxylation, phosphorylation, or glycosylation, and such modifications may occur during polypeptide synthesis or processing or following treatment with isolated modifying enzymes. In particular, orthologs of the invention will generally exhibit at least 80-85%, more preferably 90%, and most preferably 95%, 96%, 97%, 98% or even 99% identity or homology with all or part of a naturally occurring PKSRP amino acid sequence and will exhibit a function similar to a PKSRP. Orthologs of the present invention are also preferably capable of participating in the stress response in plants. In one embodiment, the PKSRP orthologs maintain the ability to participate in the metabolism of compounds necessary for the construction of cellular membranes in *Physcomitrella patens*, or in the transport of molecules across these membranes.

In addition to naturally-occurring variants of a PKSRP sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into a nucleotide sequence of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26, thereby leading to changes in the amino acid sequence of the encoded PKSRP, without altering the functional ability of the PKSRP. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the PKSRPs without altering the activity of said PKSRP, whereas an "essential" amino acid residue is required for PKSRP activity. Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having PKSRP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering PKSRP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding PKSRPs that contain changes in amino acid residues that are not essential for PKSRP activity. Such PKSRPs differ in amino acid sequence from a sequence contained in SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 or SEQ ID NO:39, yet retain at least one of the PKSRP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39, more preferably at least about 60-70% homologous to one of the sequences of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39. The preferred PKSRP homologs of the present invention are preferably capable of participating in the a stress tolerance response in a plant, or more particularly, participating in the transcription of a protein involved in a stress tolerance response in a *Physcomitrella patens* plant, or have one or more activities set forth in Table 1.

An isolated nucleic acid molecule encoding a PKSRP homologous to a protein sequence of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 or SEQ ID NO:39 can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26 such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations

can be introduced into one of the sequences of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain.

Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a PKSRP is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a PKSRP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for a PKSRP activity described herein to identify mutants that retain PKSRP activity. Following mutagenesis of one of the sequences of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26, the encoded protein can be expressed recombinantly and the activity of the protein can be determined by analyzing the stress tolerance of a plant expressing the protein as described in Example 7.

In addition to the nucleic acid molecules encoding the PKSRPs described above, another aspect of the invention pertains to isolated nucleic acid molecules that are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire PKSRP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding a PKSRP. The term "coding region" refers to the region of the nucleotide sequence comprising codons that are translated into amino acid residues (e.g., the entire coding region of , , , comprises nucleotides 1 to . . .). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding a PKSRP. The term "noncoding region" refers to 5' and 3' sequences that flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

In a preferred embodiment, an isolated, nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26, or a portion thereof. A nucleic acid molecule that is complementary to one of the nucleotide sequences shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26 is one which is sufficiently complementary to one of the nucleotide sequences shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26 such that it can hybridize to one of the nucleotide sequences shown in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26, thereby forming a stable duplex.

Given the coding strand sequences encoding the PKSRPs disclosed herein (e.g., the sequences set forth in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of PKSRP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of PKSRP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of PKSRP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length.

An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl)uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a PKSRP to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic (including plant) promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An a-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier et al., 1987 Nucleic Acids. Res. 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al., 1987 Nucleic Acids Res. 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al., 1987 FEBS Lett. 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes described in Haselhoff and Gerlach, 1988 Nature 334:585-591) can be used to catalytically cleave PKSRP mRNA transcripts to thereby inhibit translation of PKSRP mRNA. A ribozyme having specificity for a PKSRP-encoding nucleic acid can be designed based upon the nucleotide sequence of a PKSRP cDNA, as disclosed herein (i.e., SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26) or on the basis of a heterologous sequence to be isolated according to methods taught in this invention. For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a PKSRP-encoding mRNA. See, e.g., Cecil et at. U.S. Pat. No. 4,987,071 and Cecil et al. U.S. Pat. No. 5,116,742. Alternatively, PKSRP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J. W., 1993 Science 261:1411-1418.

Alternatively, PKSRP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of a PKSRP nucleotide sequence (e.g., a PKSRP promoter and/or enhancer) to form triple helical structures that prevent transcription of a PKSRP gene in target cells. See generally, Helene, C., 1991 Anticancer Drug Des. 6(6):569-84; Helene, C. et al., 1992 Ann. N.Y. Acad. Sci. 660:27-36; and. Maher, L. J., 1992 Bioassays 14(12):807-15. 109801 In addition to the PKSRP nucleic acids and proteins described above, the present invention encompasses these nucleic acids and proteins attached to a moiety. These moieties include, but are not limited to, detection moieties, hybridization moieties, purification moieties, delivery moieties, reaction moieties, binding moieties, and the like. A typical group of nucleic acids having moieties attached are probes and primers. The probes and primers typically comprise a substantially isolated oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26, an anti-sense sequence of one of the sequences set forth in SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25 or SEQ ID NO:26 can be used in PCR reactions to clone PKSRP homologs. Probes based on the PKSRP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, e.g. the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a genomic marker test kit for identifying cells which express a PKSRP, such as by measuring a level of a PKSRP-encoding nucleic acid, in a sample of cells, e.g., detecting PKSRP mRNA levels or determining whether a genomic PKSRP gene has been mutated or deleted.

In particular, a useful method to ascertain the level of transcription of the gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel et al., 1988 Current Protocols in Molecular Biology, Wiley: N.Y.). This information at least partially demonstrates the degree of transcription of the transformed gene. Total cellular RNA can be prepared from cells, tissues or organs by several methods, all well-known in the art, such as that described in Bormann, E. R. et al., 1992 Mol. Microbiol. 6:317-326. To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed. These techniques are well known to one of ordinary skill in the art. (See, for example, Ausubel et al., 1988 Current Protocols in Molecular Biology, Wiley: N.Y.).

The invention further provides an isolated recombinant expression vector comprising a PKSRP nucleic acid as described above, wherein expression of the vector in a host cell results in increased tolerance to environmental stress as compared to a wild type variety of the host cell. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of

a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, Calif. (1990) or see: Gruber and Crosby, in: Methods in Plant Molecular Biology and Biotechnology, eds. Glick and Thompson, Chapter 7, 89-108, CRC Press: Boca Raton, Fla., including the references therein. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells and those that direct expression of the nucleotide sequence only in certain host cells or under certain conditions. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., PKSRPs, mutant forms of PKSRPs, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of PKSRPs in prokaryotic or eukaryotic cells. For example, PKSRP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M. A. et al., 1992 Foreign gene expression in yeast: a review, Yeast 8:423-488; van den Handel, C. A. M. J. J. et al., 1991 Heterologous gene expression in filamentous fungi, in: More Gene Manipulations in Fungi, J. W. Bennet & L. L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C. A. M. J. J. & Punt, P. J., 1991 Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J. F. et al., eds., p. 1-28, Cambridge University Press: Cambridge), algae (Falciatore et al., 1999 Marine Biotechnology 1(3):239-251), ciliates of the types: *Holotrichia, Peritrichia, Spirotrichia, Suctoria, Tetrahymena, Paramecium, Colpidium, Glaucoma, Platyophrya, Potomacus, Pseudocohnilembus, Euplotes, Engelmaniella*, and *Stylonychia*, especially of the genus *Stylonychia lemnae* with vectors following a transformation method as described in WO 98/01572 and multicellular plant cells (see Schmidt, R. and Willmitzer, L., 1988 High efficiency *Agrobacterium tumefaciens*-mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants, Plant Cell Rep. 583-586); Plant Molecular Biology and Biotechnology, C Press, Boca Raton, Fla., chapter 6/7, S.71-119 (1993); F. F. White, B. Jenes et al, Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds. Kung and R. Wu, 128-43, Academic Press: 1993; Pottykus, 1991 Annu. Rev. Plant Physiol. Plant Molec. Biol. 42:205-225 and references cited therein) or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press: San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated in vitro, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of a recombinant protein; 2) to increase the solubility of a recombinant protein; and 3) to aid in the purification of a recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D. B. and Johnson, K. S., 1988 Gene 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the PKSRP is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant PKSRP unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann et al., 1988 Gene 69:301-315) and pET 11d (Studier et al., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, Calif. (1990) 60-89). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, Calif. (1990) 119-128). Another strategy is to alter the sequence of the

nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada et al., 1992 Nucleic Acids Res. 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the PKSRP expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, et al., 1987 Embo J. 6:229-234), pMFa (Kurjan and Herskowitz, 1982 Cell 30:933-943), pJRY88 (Schultz et al., 1987 Gene 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, Calif.). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C. A. M. J. J. & Punt, P. J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J. F. Peberdy, et al., eds., p. 1-28, Cambridge University Press: Cambridge.

Alternatively, the PKSRPs of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith et al., 1983 Mol. Cell Biol. 3:2156-2165) and the pVL series (Lucklow and Summers, 1989 Virology 170:31-39).

In yet another embodiment, a PKSRP nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B., 1987 Nature 329:840) and pMT2PC (Kaufman et al., 1987 EMBO J. 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert et al., 1987 Genes Dev. 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988 Adv. Immunol. 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989 EMBO J. 8:729-733) and immunoglobulins (Banerji et al., 1983 Cell 33:729-740; Queen and Baltimore, 1983 Cell 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, 1989 *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund et al., 1985 Science 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example, the murine hox promoters (Kessel and Gruss, 1990 Science 249:374-379) and the fetoprotein promoter (Campes and Tilghman, 1989 Genes Dev. 3:537-546).

In another embodiment, the PKSRPs of the invention may be expressed in unicellular plant cells (such as algae) (see Faleiatore et al., 1999 Marine Biotechnology 1(3):239-251 and references therein) and plant cells from higher plants (e.g., the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R., 1992 New plant binary vectors with selectable markers located proximal to the left border, Plant Mol. Biol, 20: 1195-1197; and Bevan, M. W., 1984 Binary *Agrobacterium* vectors for plant transformation, Nucl. Acid. Res. 12:8711-8721; Vectors for Gene Transfer in Higher Plants; in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds.: Kung and R. Wu, Academic Press, 1993, S. 15-38.

A plant expression cassette preferably contains regulatory sequences capable of driving gene expression in plant cells and operably linked so that each sequence can fulfill its function, for example, termination of transcription by polyadenylation signals. Preferred polyadenylation signals are those originating from *Agrobacterium tumefaciens* t-DNA such as the gene 3 known as octopine synthase of the Ti-plasmid pTiACH5 (Gielen et al., 1984 EMBO J. 3:835) or functional equivalents thereof but also all other terminators functionally active in plants are suitable,

As plant gene expression is very often not limited on transcriptional levels, a plant expression cassette preferably contains other operably linked sequences like translational enhancers such as the overdrive-sequence containing the 5'-untranslated leader sequence from tobacco mosaic virus enhancing the protein per RNA ratio (Gallie et al., 1987 Nucl. Acids Research 15:8693-8711).

Plant gene expression has to be operably linked to an appropriate promoter conferring gene expression in a timely, cell or tissue specific manner. Preferred are promoters driving constitutive expression (Benfey et al., 1989 EMBO J. 8:2195-2202) like those derived from plant viruses like the 35S CAMV (Franck et al., 1980 Cell 21:285-294), the 19S CaMV (see also U.S. Pat. No. 5,352,605 and PCT Application No, WO 8402913) or plant promoters like those from Rubisco small subunit described in U.S. Pat. No. 4,962,028.

Other preferred sequences for use in plant gene expression cassettes are targeting-sequences necessary to direct the gene product in its appropriate cell compartment (for review see Kermode, 1996 Crit. Rev, Plant Sci. 15(4):285-423 and references cited therein) such as the vacuole, the nucleus, all types of plastids like amyloplasts, chloroplasts, chromoplasts, the extracellular space, mitochondria, the endoplasmic reticulum, oil bodies, peroxisomes and other compartments of plant cells.

Plant gene expression can also be facilitated via an inducible promoter (for review see Gatz, 1997 Annu. Rev. Plant Physiol. Plant Mol. Biol. 48:89-108). Chemically inducible promoters are especially suitable if gene expression is wanted to occur in a time specific manner. Examples of such promoters are a salicylic acid inducible promoter (PCT Application No. WO 95/19443), a tetracycline inducible promoter (Gatz et al., 1992 Plant J. 2:397-404) and an ethanol inducible promoter (PCT Application No. WO 93/21334).

Also, suitable promoters responding to biotic or abiotic stress conditions are those such as the pathogen inducible PRP1-gene promoter (Ward et al., 1993 Plant. Mol. Biol. 22:361-366), the heat inducible hsp80-promoter from tomato (U.S. Pat. No. 5,187,267), cold inducible alpha-amylase promoter from potato (PCT Application No. WO 96/12814) or the wound-inducible pinII-promoter (European Patent No. 375091). For other examples of drought, cold, and salt-inducible promoters, such as the RD29A promoter, see Yamaguchi-Shinozalei et al. (1993 Mol. Gen. Genet, 236:331-340).

Especially preferred are those promoters that confer gene expression in specific tissues and organs, such as guard cells and the root hair cells. Suitable promoters include the napin-gene promoter from rapeseed (U.S. Pat. No. 5,608,152), the

USP-promoter from *Vicia faba* (Baeumlein et al., 1991 Mol Gen Genet. 225(3):459-67), the oleosin-promoter from *Arabidopsis* (PCT Application No. WO 98/45461), the phaseolin-promoter from Phaseolus vulgaris (U.S. Pat. No. 5,504,200), the Bce4-promoter from Brassica (PCT Application No. WO 91/13980) or the legumin B4 promoter (LeB4; Baeumlein et al., 1992 Plant Journal, 2(2)233-9) as well as promoters conferring seed specific expression in monocot plants like maize, barley, wheat, rye, rice, etc. Suitable promoters to note are the lpt2 or lpt1-gene promoter from barley (PCT Application No. WO 95/15389 and PCT Application No. WO 95/23230) or those described in PCT Application No. WO 99/16890 (promoters from the barley hordein-gene, rice glutelin gene, rice oryzin gene, rice prolamin gene, wheat gliadin gene, wheat glutelin gene, maize zein gene, oat glutelin gene, Sorghum kasirin-gene and rye secalin gene).

Also especially suited are promoters that confer plastid-specific gene expression since plastids are the compartment where lipid biosynthesis occurs. Suitable promoters are the viral RNA-polymerase promoter described in PCT Application No. WO 95/16783 and PCT Application No, WO 97/06250 and the clpP-promoter from *Arabidopsis* described in PCT Application No. WO 99/46394.

The invention further provides a recombinant expression vector comprising a PKSRP DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to a PKSRP mRNA. Regulatory sequences operatively linked to a nucleic acid molecule cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types. For instance, viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus wherein antisense nucleic acids are produced under the control of a high efficiency regulatory region. The activity of the regulatory region can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. et al., Antisense RNA as a molecular tool for genetic analysis, Reviews-Trends in Genetics, Vol. 1(1) 1986 and Mol et al., 1990 FEBS Letters 268:427-430.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but they also apply to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a PKSRP can be expressed in bacterial cells such as *C. glutamicum*, insect cells, fungal cells or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells), algae, ciliates, plant cells, fungi or other microorganisms like *C. glutamicum*. Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation", "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAF-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer and electroporation. Suitable methods for transforming or transfecting host cells including plant cells can be found in Sambrook, et al. (Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989) and other laboratory manuals such as Methods in Molecular Biology, 1995, Vol, 44, *Agrobacterium* protocols, ed: Gartland and Davey, Humana Press, Totowa, N.J. As biotic and abiotic stress tolerance is a general trait wished to be inherited into a wide variety of plants like maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed and canola, manihot, pepper, sunflower and tagetes, solanaceous plants like potato, tobacco, eggplant, and tomato, Vicia species, pea, alfalfa, bushy plants (coffee, cacao, tea), Salix species, trees (oil palm, coconut), perennial grasses and forage crops, these crop plants are also preferred target plants for a genetic engineering as one further embodiment of the present invention,

In particular, the invention provides a method of producing a transgenic plant with a PKSRP coding nucleic acid, wherein expression of the nucleic acid(s) in the plant results in increased tolerance to environmental stress as compared to a wild type variety of the plant comprising: (a) transforming a plant cell with an expression vector comprising a PKSRP nucleic acid, and (b) generating from the plant cell a transgenic plant with a increased tolerance to environmental stress as compared to a wild type variety of the plant. The invention also provides a method of increasing expression of a gene of interest within a host cell as compared to a wild type variety of the host cell, wherein the gene of interest is transcribed in response to a PKSRP, comprising: (a) transforming the host cell with an expression vector comprising a PKSRP coding nucleic acid, and (b) expressing the PKSRP within the host cell, thereby increasing the expression of the gene transcribed in response to the PKSRP, as compared to a wild type variety of the host cell.

For such plant transformation, binary vectors such as pBinAR can be used (Höfgen and Willmitzer, 1990 Plant Science 66:221-230). Construction of the binary vectors can be performed by ligation of the cDNA in sense or antisense orientation into the T-DNA. 5-prime to the cDNA a plant promoter activates transcription of the cDNA. A polyadenylation sequence is located 3-prime to the cDNA. Tissue-specific expression can be achieved by using a tissue specific promoter. For example, seed-specific expression can be achieved by cloning the napin or LeB4 or USP promoter 5-prime to the cDNA. Also, any other seed specific promoter element can be used. For constitutive expression within the whole plant, the CaMV 35S promoter can be used. The expressed protein can be targeted to a cellular compartment using a signal peptide, for example for plastids, mitochondria or endoplasmic reticulum (Kermode, 1996 Crit. Rev. Plant Sci. 4(15):285-423). The signal peptide is cloned 5-prime in frame to the cDNA to archive subcellular localization of the fusion protein. Additionally, promoters that are responsive to abiotic stresses can be used with, such as the *Arabidopsis* promoter RD29A, the nucleic acid sequences disclosed herein. One skilled in the art will recognize that the promoter used should be operatively linked to the nucleic acid such that the promoter causes transcription of the nucleic acid which results in the synthesis of an mRNA which encodes a polypeptide. Alternatively, the

RNA can be an antisense RNA for use in affecting subsequent expression of the same or another gene or genes.

Alternate methods of transfection include the direct transfer of DNA into developing flowers via electroporation or *Agrobacterium* mediated gene transfer. *Agrobacterium* mediated plant transformation can be performed using for example the GV3101(pMP90) (Koncz and Schell, 1986 Mol. Gen. Genet. 204:383-396) or LBA4404 (Clontech) *Agrobacterium tumefaciens* strain. Transformation can be performed by standard transformation and regeneration techniques (Deblaere et al., 1994 Nucl. Acids. Res. 13:4777-4788; Gelvin, Stanton B. and Schilperoort, Robert A, Plant Molecular Biology Manual, 2nd Ed.—Dordrecht: Kluwer Academic Publ., 1995.—in Sect., Ringbuc Zentrale Signatur: BT11-P ISBN 0-7923-2731-4; Glick, Bernard R.; Thompson, John E., Methods in Plant Molecular Biology and Biotechnology, Boca Raton: CRC Press, 1991 - 360 S., ISBN 0-8493-5164-2). For example, rapeseed can be transformed via cotyledon or hypocotyl transformation (Moloney et al., 1989 Plant cell Report 8:238-242; De Block et al., 1989 Plant Physiol. 91:694-701). Use of antibiotica for *Agrobacterium* and plant selection depends on the binary vector and the *Agrobacterium* strain used for transformation. Rapeseed selection is normally performed using kanamycin as selectable plant marker. *Agrobacterium* mediated gene transfer to flax can be performed using, for example, a technique described by Mlynarova et al., 1994 Plant Cell Report 13:282-285. Additionally, transformation of soybean can be performed using for example a technique described in European Patent No. 0424 047, U.S. Pat. No. 5,322,783, European Patent No. 0397 687, U.S. Pat. Nos. 5,376,543 or 5,169,770. Transformation of maize can be achieved by particle bombardment, polyethylene glycol mediated DNA uptake or via the silicon carbide fiber technique. (See, for example, Freeling and Walbot "The maize handbook" Springer Verlag: New York (1993) ISBN 3-540-97826-7). A specific example of maize transformation is found in U.S. Pat. No. 5,990,387 and a specific example of wheat transformation can be found in PCT Application No. WO 93/07256.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate or in plants that confer resistance towards a herbicide such as glyphosate or glufosinate. Nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector as that encoding a PKSRP or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be identified by, for example, drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of a PKSRP gene into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the PKSRP gene. Preferably, the PKSRP gene is a *Physcomitrella patens* PKSRP gene, but it can be a homolog from a related plant or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous PKSRP gene is functionally disrupted (i.e., no longer encodes a functional protein; also referred to as a knock-out vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous PKSRP gene is mutated or otherwise altered but still encodes a functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous PKSRP). To create a point mutation via homologous recombination, DNA-RNA hybrids can be used in a technique known as chimeraplasty (Cole-Strauss et al., 1999 Nucleic Acids Research 27(5):1323-1330 and Kmiec, 1999 Gene therapy American Scientist. 87(3):240-247). Homologous recombination procedures in *Physcomitrella patens* are also well known in the art and are contemplated for use herein.

Whereas in the homologous recombination vector, the altered portion of the PKSRP gene is flanked at its 5' and 3' ends by an additional nucleic acid molecule of the PKSRP gene to allow for homologous recombination to occur between the exogenous PKSRP gene carried by the vector and an endogenous PKSRP gene, in a microorganism or plant. The additional flanking PKSRP nucleic acid molecule is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several hundreds of base pairs up to kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see e.g., Thomas, K. R., and Capecchi, M. R., 1987 Cell 51:503 for a description of homologous recombination vectors or Strepp et al., 1998 PNAS, 95 (8):4368-4373 for cDNA based recombination in *Physcomitrella patens*). The vector is introduced into a microorganism or plant cell (e.g., via polyethylene glycol mediated DNA), and cells in which the introduced PKSRP gene has homologously recombined with the endogenous PKSRP gene are selected using art-known techniques.

In another embodiment, recombinant microorganisms can be produced that contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of a PKSRP gene on a vector placing it under control of the lac operon permits expression of the PKSRP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

A host cell of the invention, such as a prokaryotic or eukaryotie host cell in culture, can be used to produce (i.e., express) a PKSRP. Accordingly, the invention further provides methods for producing PKSRPs using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a PKSRP has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered PKSRP) in a suitable medium until PKSRP is produced. In another embodiment, the method further comprises isolating PKSRPs from the medium or the host cell.

Another aspect of the invention pertains to isolated PKSRPs, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is free of some of the cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of PKSRP in which the protein is separated from some of the cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of a PKSRP having less than about 30% (by dry weight) of non-PKSRP material (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-PKSRP material, still more preferably less than about 10% of non-PKSRP material, and most preferably less than about 5% non-PKSRP material.

When the PKSRP or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of PKSRP in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of a PKSRP having less than about 30% (by dry weight) of chemical precursors or non-PKSRP chemicals, more preferably less than about 20% chemical precursors or non-PKSRP chemicals, still more preferably less than about 10% chemical precursors or non-PKSRP chemicals, and most preferably less than about 5% chemical precursors or non-PKSRP chemicals. In preferred embodiments, isolated proteins, or biologically active portions thereof, lack contaminating proteins from the same organism from which the PKSRP is derived. Typically, such proteins are produced by recombinant expression of, for example, a *Physcomitrella patens* PKSRP in plants other than *Physcomitrella patens* or microorganisms such as *C. glutamicum*, ciliates, algae or fungi.

The nucleic acid molecules, proteins, protein homologs, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *Physcomitrella patens* and related organisms; mapping of genomes of organisms related to *Physcomitrella patens*; identification and localization of *Physcomitrella patens* sequences of interest; evolutionary studies; determination of PKSRP regions required for function; modulation of a PKSRP activity; modulation of the metabolism of one or more cell functions; modulation of the transmembrane transport of one or more compounds; and modulation of stress resistance.

The moss *Physcomitrella patens* represents one member of the mosses. It is related to other mosses such as *Ceratodon purpureus* which is capable of growth in the absence of light. Mosses like *Ceratodon* and *Physcomitrella* share a high degree of homology on the DNA sequence and polypeptide level allowing the use of heterologous screening of DNA molecules with probes evolving from other mosses or organisms, thus enabling the derivation of a consensus sequence suitable for heterologous screening or functional annotation and prediction of gene functions in third species. The ability to identify such functions can therefore have significant relevance, e.g., prediction of substrate specificity of enzymes. Further, these nucleic acid molecules may serve as reference points for the mapping of moss genomes, or of genomes of related organisms.

The PKSRP nucleic acid molecules of the invention have a variety of uses. Most importantly, the nucleic acid and amino acid sequences of the present invention can be used to transform plants, thereby inducing tolerance to stresses such as drought, high salinity and cold. The present invention therefore provides a transgenic plant transformed by a PKSRP nucleic acid (coding or antisense), wherein expression of the nucleic acid sequence in the plant results in increased tolerance to environmental stress as compared to a wild type variety of the plant. The transgenic plant can be a monocot or a dicot. The invention further provides that the transgenic plant can be selected from maize, wheat, lye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix* species, oil palm, coconut, perennial grass and forage crops, for example.

In particular, the present invention describes using the expression of PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2 of *Physcomitrella patens* to engineer drought-tolerant, salt-tolerant and/or cold-tolerant plants. This strategy has herein been demonstrated for *Arabidopsis thaliana*, Rapeseed/Canola, soybeans, corn and wheat but its application is not restricted to these plants. Accordingly, the invention provides a transgenic plant containing a PKSRP selected from PK-6 (SEQ ID NO:27), PK-7 (SEQ ID NO:28), PK-8 (SEQ ID NO:29), PK-9 (SEQ ID NO:30), CK-1 (SEQ ID NO:31), CK-2 (SEQ ID NO:32), CK-3 (SEQ ID NO:33), MPK-2 (SEQ ID NO:34), MPK-3 (SEQ ID NO:35), MPK-4 (SEQ ID NO:36), MPK-5 (SEQ ID NO:37), CPK-1 (SEQ ID NO:38) and CPK-2 (SEQ ID NO:39), wherein the environmental stress is drought, increased salt or decreased or increased temperature. In preferred embodiments, the environmental stress is drought or decreased temperature.

The present invention also provides methods of modifying stress tolerance of a plant comprising, modifying the expression of a PKSRP in the plant. The invention provides that this method can be performed such that the stress tolerance is either increased or decreased. In particular, the present invention provides methods of producing a transgenic plant having an increased tolerance to environmental stress as compared to a wild type variety of the plant comprising increasing expression of a PKSRP in a plant.

The methods of increasing expression of PKSRPs can be used wherein the plant is either transgenic or not transgenic. In cases when the plant is transgenic, the plant can be transformed with a vector containing any of the above described PKSRP coding nucleic acids, or the plant can be transformed with a promoter that directs expression of native PKSRP in the plant, for example. The invention provides that such a promoter can be tissue specific. Furthermore, such a promoter can be developmentally regulated. Alternatively, non-transgenic plants can have native PKSRP expression modified by inducing a native promoter.

The expression of PK-6 (SEQ ID NO:14), PK-7 (SEQ ID NO:15), PK-8 (SEQ ID NO:16), PK-9 (SEQ ID NO:17), CK-1 (SEQ ID NO:18), CK-2 (SEQ ID NO:19), CK-3 (SEQ ID NO:20), MPK-2 (SEQ ID NO:21), MPK-3 (SEQ ID NO:22), MPK-4 (SEQ ID NO:23), MPK-5 (SEQ ID NO:24), CPK-1 (SEQ ID NO:25) and CPK-2 (SEQ ID NO:26) in target plants can be accomplished by, but is not limited to, one of the following examples: (a) constitutive promoter, (b) stress-inducible promoter, (c) chemical-induced promoter, and (d) engineered promoter over-expression with for example zinc-finger derived transcription factors (Greisman and Pabo, 1997 Science 275:657). The later case involves identification of the PK-6 (SEQ ID NO:27), PK-7 (SEQ ID NO:28), PK-8 (SEQ ID NO:29), PK-9 (SEQ ID NO:30), CK-1 (SEQ ID NO:31), CK-2 (SEQ ID NO:32), CK-3 (SEQ ID NO:33), MPK-2 (SEQ ID NO:34), MPK-3 (SEQ ID NO:35), MPK-4 (SEQ ID NO:36), MPK-5 (SEQ ID NO:37), CPK-1 (SEQ ID NO:38) or CPK-2 (SEQ ID NO:39) homologs in the target plant as well as from its promoter. Zinc-finger-containing recombinant transcription factors are engineered to specifically interact with the PK-6 (SEQ ID NO:27), PK-7 (SEQ ID NO:28), PK-8 (SEQ ID NO:29), PK-9 (SEQ ID NO:30), CK-1 (SEQ ID NO:31), CK-2 (SEQ ID NO:32), CK-3 (SEQ ID NO:33), MPK-2 (SEQ ID NO:34), MPK-3 (SEQ ID NO:35), MPK-4 (SEQ ID NO:36),

MPK-5 (SEQ ID NO:37), CPK-1 (SEQ ID NO:38) or CPK-2 (SEQ ID NO:39) homolog and transcription of the corresponding gene is activated.

In addition to introducing the PKSRP nucleic acid sequences into transgenic plants, these sequences can also be used to identify an organism as being *Physcomitrella patens* or a close relative thereof. Also, they may be used to identify the presence of *Physcomitrella patens* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *Physcomitrella patens* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *Physcomitrella patens* gene which is unique to this organism, one can ascertain whether this organism is present.

Further, the nucleic acid and protein molecules of the invention may serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also in functional studies of *Physcomitrella patens* proteins. For example, to identify the region of the genome to which a particular *Physcomitrella patens* DNA-binding protein binds, the *Physcomitrella patens* genome could be digested, and the fragments incubated with the DNA-binding protein. Those fragments that bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels. Binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *Physcomitrella patens*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related mosses,

The PKSRP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and transport processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein that are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the PKSRP nucleic acid molecules of the invention may result in the production of PKSRPs having functional differences from the wild-type PKSRPs. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

There are a number of mechanisms by which the alteration of a PKSRP of the invention may directly affect stress response and/or stress tolerance. In the case of plants expressing PKSRPs, increased transport can lead to improved salt and/or solute partitioning within the plant tissue and organs. By either increasing the number or the activity of transporter molecules which export ionic molecules from the cell, it may be possible to affect the salt tolerance of the cell.

The effect of the genetic modification in plants, *C. glutainicum*, fungi, algae, or ciliates on stress tolerance can be assessed by growing the modified microorganism or plant under less than suitable conditions and then analyzing the growth characteristics and/or metabolism of the plant. Such analysis techniques are well known to one skilled in the art, and include dry weight, wet weight, protein synthesis, carbohydrate synthesis, lipid synthesis, evapotranspiration rates, general plant and/or crop yield, flowering, reproduction, seed setting, root growth, respiration rates, photosynthesis rates, etc. (Applications of HPLC in Biochemistry in Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm et al., 1993 Biotechnology, vol. 3, Chapter III: Product recovery and purification, page 469-714, VCH: Weinheim; Belter, P. A. et al., 1988 Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J. F. and Cabral, J. M. S., 1992 Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J. A. and Hemy, J. D., 1988 Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F. J. (1989) Separation and purification techniques in biotechnology, Noyes Publications).

For example, yeast expression vectors comprising the nucleic acids disclosed herein, or fragments thereof, can be constructed and transformed into *Saccharomyces cerevisiae* using standard protocols. The resulting transgenic cells can then be assayed for fail or alteration of their tolerance to drought, salt, and temperature stress. Similarly, plant expression vectors comprising the nucleic acids disclosed herein, or fragments thereof, can be constructed and transformed into an appropriate plant cell such as *Arabidopsis* , soy, rape, maize, wheat, *Medicago truncatula*, etc., using standard protocols. The resulting transgenic cells and/or plants derived there from can then be assayed for fail or alteration of their tolerance to drought, salt, and temperature stress.

The engineering of one or more PKSRP genes of the invention may also result in PKSRPs having altered activities which indirectly impact the stress response and/or stress tolerance of algae, plants, ciliates or fungi or other microorganisms like *C. glutamicum*. For example, the normal biochemical processes of metabolism result in the production of a variety of products (e.g., hydrogen peroxide and other reactive oxygen species) which may actively interfere with these same metabolic processes (for example, peroxynitrite is known to nitrate tyrosine side chains, thereby inactivating some enzymes having tyrosine in the active site (Groves, J. T., 1999 Curr. Opin. Chem. Biol. 3(2):226-235). While these products are typically excreted, cells can be genetically altered to transport more products than is typical for a wild-type cell. By optimizing the activity of one or more PKSRPs of the invention which are involved in the export of specific molecules, such as salt molecules, it may be possible to improve the stress tolerance of the cell.

Additionally, the sequences disclosed herein, or fragments thereof, can be used to generate knockout mutations in the genomes of various organisms, such as bacteria, mammalian cells, yeast cells, and plant cells (Girke, T., 1998 The Plant Journal 15:39-48). The resultant knockout cells can then be evaluated for their ability or capacity to tolerate various stress conditions, their response to various stress conditions, and the effect on the phenotype and/or genotype of the mutation. For other methods of gene inactivation see U.S. Pat. No. 6,004,804 "Non-Chimeric Mutational Vectors" and Puttaraju et al., 1999 Spliceosome-mediated RNA trans-splicing as a tool for gene therapy Nature Biotechnology 17:246-252.

The aforementioned mutagenesis strategies for PKSRPs resulting in increased stress resistance are not meant to be limiting; variations on these strategies will be readily apparent to one skilled in the art. Using such strategies, and incor-

porating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate algae, ciliates, plants, fungi or other microorganisms like *C. glutamicum* expressing mutated PKSRP nucleic acid and protein molecules such that the stress tolerance is improved.

The present invention also provides antibodies that specifically bind to a PKSRP, or a portion thereof, as encoded by a nucleic acid described herein. Antibodies can be made by many well-known methods (See, e.g. Harlow and Lane, "Antibodies; A Laboratory Manual" Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., (1988)). Briefly, purified antigen can be injected into an animal in an amount and in intervals sufficient to elicit an immune response. Antibodies can either be purified directly, or spleen cells can be obtained from the animal. The cells can then fused with an immortal cell line and screened for antibody secretion. The antibodies can be used to screen nucleic acid clone libraries for cells secreting the antigen. Those positive clones can then be sequenced. (See, for example, Kelly et al., 1992 Bio/Technology 10:163-167; Bebbington et al., 1992 Bio/Technology 10:169-175).

The phrases "selectively binds" and "specifically binds" with the polypeptide refer to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bound to a particular protein do not bind in a significant amount to other proteins present in the sample. Selective binding of an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. A variety of immunoassay formats may be used to select antibodies that selectively bind with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies selectively immunoreactive with a protein. See Harlow and Lane "Antibodies, A Laboratory Manual" Cold Spring Harbor Publications, New York, (1988), for a description of immunoassay formats and conditions that could be used to determine selective binding.

In some instances, it is desirable to prepare monoclonal antibodies from various hosts. A description of techniques for preparing such monoclonal antibodies may be found in Stites et al., editors, "Basic and Clinical Immunology," (Lange Medical Publications, Los Altos, Calif., Fourth Edition) and references cited therein, and in Harlow and Lane ("Antibodies, A Laboratory Manual" Cold Spring Harbor Publications, New York, 1988).

Throughout this application, various publications are referenced. The disclosures of all of these publications and those references cited within those publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

It should also be understood that the foregoing relates to preferred embodiments of the present invention and that numerous changes may be made therein without departing from the scope of the invention. The invention is further illustrated by the following examples, which are not to be construed in any way as imposing limitations upon the scope thereof. On the contrary, it is to be clearly understood that resort may be had to various other embodiments, modifications, and equivalents thereof; which, after reading the description herein, may suggest themselves to those skilled in the art without departing from the spirit of the present invention and/or the scope of the appended claims.

EXAMPLES

Example 1

Growth of *Physcomitrella Patens* Cultures

For this study, plants of the species *Physcomitrella patens* (Hedw.) B.S.G. from the collection of the genetic studies section of the University of Hamburg were used. They originate from the strain 16/14 collected by H. L. K. Whitehouse in Gransden Wood, Huntingdonshire (England), which was subcultured from a spore by Engel (1968, Am. J. Bot. 55, 438-446). Proliferation of the plants was carried out by means of spores and by means of regeneration of the gametophytes. The protonema developed from the haploid spore as a chloroplast-rich chloronema and chloroplast-low caulonema, on which buds formed after approximately 12 days. These grew to give gametophores bearing antheridia and archegonia. After fertilization, the diploid sporophyte with a short seta and the spore capsule resulted, in which the meiospores matured.

Culturing was carried out in a climatic chamber at an air temperature of 25° C. and light intensity of 55 micromol s^{-1} m^{-2} (white light; Philips TL 65W/25 fluorescent tube) and a light/dark change of 16/8 hours. The moss was either modified in liquid culture using Knop medium according to Reski and Abel (1985, Planta 165:354-358) or cultured on Knop solid medium using 1% oxoid agar (Unipath, Basingstoke, England). The protonemas used for RNA and DNA isolation were cultured in aerated liquid cultures. The protonemas were comminuted every 9 days and transferred to fresh culture medium.

Example 2

Total DNA Isolation from Plants

The details for the isolation of total DNA relate to the working up of one gram fresh weight of plant material. The materials used include the following buffers: CTAB buffer: 2% (w/v) N-cethyl-N,N,N-trimethylammonium bromide (CTAB); 100 mM Tris HCl pH 8.0; 1.4 M NaCl; 20 mM EDTA; N-Laurylsarcosine buffer: 10% (w/v) N-laurylsarcosine; 100 mM Tris HCl pH 8.0; 20 mM EDTA.

The plant material was triturated under liquid nitrogen in a mortar to give a fine powder and transferred to 2 ml Eppendorf vessels. The frozen plant material was then covered with a layer of 1 ml of decomposition buffer (1 ml CTAB buffer, 100 µl of N-laurylsarcosine buffer, 20 µl of β-mercaptoethanol and 10 µl of proteinase K solution, 10 mg/ml) and incubated at 60° C. for one hour with continuous shaking. The homogenate obtained was distributed into two Eppendorf vessels (2 ml) and extracted twice by shaking with the same volume of chloroform/isoamyl alcohol (24:1). For phase separation, centrifugation was carried out at 8000×g and room temperature for 15 minutes in each case. The DNA was then precipitated at −70° C. for 30 minutes using ice-cold isopropanol. The precipitated DNA was sedimented at 4° C. and 10,000 g for 30 minutes and resuspended in 180 µl of TE buffer (Sambrook et al., 1989, Cold Spring Harbor Laboratory Press: ISBN 0-87969-309-6). For further purification, the DNA was treated with NaCl (1.2 M final concentration) and precipitated again at −70° C. for 30 minutes using twice the volume of absolute ethanol. After a washing step with 70% ethanol, the DNA was dried and subsequently taken up in 50 µl of H_2O+RNAse (50 mg/ml final concentration). The DNA was dissolved overnight at 4° C. and the RNAse digestion was subsequently carried out at 37° C. for 1 hour, Storage of the DNA took place at 4° C.

Example 3

Isolation of Total RNA and poly-(A)+ RNA and cDNA Library Construction from *Physcomitrella Patens*

For the investigation of transcripts, both total RNA and poly-$(A)^+$ RNA were isolated. The total RNA was obtained from wild-type 9 day old protonemata following the GTC-method (Reski et al. 1994, Mol. Gen. Genet., 244:352-359). The Poly(A)+ RNA was isolated using Dyna Beads^R (Dynal, Oslo, Norway) following the instructions of the manufacturers protocol. After determination of the concentration of the RNA or of the poly(A)+ RNA, the RNA was precipitated by addition of 1/10 volumes of 3 M sodium acetate pH 4.6 and 2 volumes of ethanol and stored at −70° C.

For cDNA library construction, first strand synthesis was achieved using Murine Leukemia Virus reverse transcriptase (Roche, Mannheim, Germany) and oligo-d(T)-primers, second strand synthesis by incubation with DNA polymerase I, Klenow enzyme and RNAseH digestion at 12° C. (2 hours), 16° C. (1 hour) and 22° C. (1 hour). The reaction was stopped by incubation at 65° C. (10 minutes) and subsequently transferred to ice. Double stranded DNA molecules were blunted by T4-DNA-polymerase (Roche, Mannheim) at 37° C. (30 minutes). Nucleotides were removed by phenol/chloroform extraction and Sephadex G50 spin columns. EcoRI adapters (Pharmacia, Freiburg, Germany) were ligated to the cDNA ends by T4-DNA-ligase (Roche, 12° C., overnight) and phosphmlated by incubation with polynucleotide kinase (Roche, 37° C., 30 minutes). This mixture was subjected to separation on a low melting agarose gel. DNA molecules larger than 300 base pairs were eluted from the gel, phenol extracted, concentrated on Elutip-D-columns (Schleicher and Schuell, Dassel, Germany) and were ligated to vector arms and packed into lambda ZAPII phages or lambda ZAP-Express phages using the Gigapack Gold Kit (Stratagene, Amsterdam, Netherlands) using material and following the instructions of the manufacturer.

Example 4

Sequencing and Function Annotation of *Physcomitrella Patens* ESTs

cDNA libraries as described in Example 3 were used for DNA sequencing according to standard methods, and in particular, by the chain termination method using the ABI PRISM Big Dye Terminator Cycle Sequencing Ready Reaction Kit (Perkin-Elmer, Weiterstadt, Germany). Random Sequencing was carried out subsequent to preparative plasmid recovery from cDNA libraries via in vivo mass excision, retransformation, and subsequent plating of DH10B on agar plates (material and protocol details from Stratagene, Amsterdam, Netherlands. Plasmid DNA was prepared from overnight grown *E. coli* cultures grown in Luria-Broth medium containing ampicillin (see Sambrook et al. 1989 Cold Spring Harbor Laboratory Press: ISBN 0-87969-309-6) on a Qiagene DNA preparation robot (Qiagen, Hilden) according to the manufacturer's protocols. Sequencing primers with the following nucleotide sequences were used:

5'-CAGGAAACAGCTATGACC-3'	SEQ ID NO: 40
5'-CTAAAGGGAACAAAAGCTG-3'	SEQ ID NO: 41
5'-TGTAAAACGACGGCCAGT-3'	SEQ ID NO: 42

Sequences were processed and annotated using the software package EST-MAX commercially provided by Bio-Max (Munich, Germany). The program incorporates practically all bioinformatics methods important for functional and structural characterization of protein sequences. For reference the website at pedant.nzips.biochem.mpg.de. The most important algorithms incorporated in EST-MAX are: FASTA: Very sensitive sequence database searches with estimates of statistical significance; Pearson W. R. (1990) Rapid and sensitive sequence comparison with FASTP and FASTA. Methods Enzymol. 183:63-98; BLAST: Very sensitive sequence database searches with estimates of statistical significance. Altschul S. F., Gish W., Miller W., Myers E. W., and Lipman D. J. Basic local alignment search tool. Journal of Molecular Biology 215:403-10; PREDATOR: High-accuracy secondary structure prediction from single and multiple sequences. Frishman, D. and Argos, P. (1997) 75% accuracy in protein secondary structure prediction. Proteins, 27:329-335; CLUSTALW: Multiple sequence alignment. Thompson, J. D., Higgins, D. G. and Gibson, T. J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. Nucleic Acids Research, 22:4673-4680; TMAP: Transmembrane region prediction from multiply aligned sequences. Persson, B. and Argos, P. (1994) Prediction of transmembrane segments in proteins utilizing multiple sequence alignments. J. Mol. Biol. 237:182-192; ALOM2: Transmembrane region prediction from single sequences. Klein, P., Kanehisa, M., and DeLisi, C. Prediction of protein function from sequence properties: A discriminate analysis of a database, Biochim, Biophys. Acta 787:221-226 (1984). Version 2 by Dr. K. Nakai; PROSEARCH: Detection of PROSITE protein sequence patterns. Kolakowski L. F. Jr., Leunissen J. A. M., Smith J. E. (1992) ProSearch: fast searching of protein sequences with regular expression patterns related to protein structure and function. Biotechniques 13, 919-921; BLIMPS: Similarity searches against a database of ungapped blocks, J. C. Wallace and Henikoff S., (1992); PATMAT: A searching and extraction program for sequence, pattern and block queries and databases, CABIOS 8:249-254. Written by Bill Alford.

Example 5

Identification of *Physcomitrella Patens* ORFS Corresponding to PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-4, MPK-5, CPK-1 and CPK-2

The *Physcomitrella patens* partial eDNAs (ESTs) shown in Table 1 below were identified in the *Physcomitrella patens* EST sequencing program using the program EST-MAX through BLAST analysis. The Sequence Identification Numbers corresponding to these ESTs are as follows: PK-6 (SEQ ID NO:1), PK-7 (SEQ ID NO:2), PK-8 (SEQ ID NO:3), PK-9 (SEQ ID NO:4), CK-1 (SEQ ID NO:5), CK-2 (SEQ ID NO:6), CK-3 (SEQ ID NO:7), MPK-2 (SEQ ID NO:8), MPK-3 (SEQ ID NO:9), MPK-4 (SEQ ID NO:10), MPK-5 (SEQ ID NO:11), CPK-1 (SEQ ID NO:12) and CPK-2 (SEQ ID NO:13).

TABLE 1

Name	Functional categories	Function	Sequence code	ORF position
PpPK-6	Protein Kinase	serine/threonine protein kinase like protein	c_pp004044242r	1-474
PpPK-7	Protein Kinase	cdc2-like protein kinase cdc2MsF	s_pp001031042f	1-267
PpPK-8	Protein Kinase	protein kinase homolog F13C5.120	c_pp004044100r	1-581
PpPK-9	Protein Kinase	protein kinase; similar to human PKX1	c_pp004071077r	709-137
PpCK-1	Protein Kinase	receptor protein kinase	c_pp001062017r	1160-1
PpCK-2	Protein Kinase	kasein kinase	c_pp004038371r	1909-1421
PpCK-3	Protein Kinase	casein kinase II catalytic subunit	c_pp004076164r	2-877
PpMPK-2	Protein Kinase	mitogen-activated protein kinase 6	c_pp004041329r	952-293
PpMPK-3	Protein Kinase	big MAP kinase 1c	c_pp004061263r	221-550
PpMPK-4	Protein Kinase	protein kinase MEK1 (EC 2.7.1.-)	c_pp001064077r	1153-596
PpMPK-5	Protein Kinase	protein kinase MEK1	c_pp004064129r	114-233
PpCPK-1	Protein Kinase	protein kinase	c_pp004014376r	1084-173
PpCPK-2	Protein Kinase	calcium-dependent protein kinase	c_pp004038141r	422-1213
PpPK-6	Protein Kinase	cdc2-like protein kinase cdc2MsF	s_pp001031042f	1-267

TABLE 2

Degree of Amino Acid Identity and Similarity of PpPK-6 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	O81106	Q9LUL4	Q9ZQZ2	Q9MAS2	Q9LK66
Protein name	LEUCINE-RICH REPEAT TRANS-MEMBRANE PROTEIN KINASE 2	SERINE/ THREONINE PROTEIN KINASE-LIKE PROTEIN	PUTATIVE LRR RECEPTOR-LINKED PROTEIN KINASE	PUTATIVE LRR RECEPTOR PROTEIN KINASE	PROTEIN KINASE-LIKE PROTEIN
Species	*Zea mays* (Maize)	*Arabidopsis thaliana* (Mouse-ear cress)	*A. thaliana*	*A. thaliana*	*A. thaliana*
Identity %	42%	42%	38%	37%	37%
Similarity %	54%	52%	50%	49%	48%

TABLE 3

Degree of Amino Acid Identity and Similarity of PpPK-7 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	P25859	O49120	Q38774	P93321	Q9ZVI4
Protein name	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG B	CYCLIN-DEPENDENT KINASE 1	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG C	CDC2 KINASE HOMOLOG CDC2MSD	PUTATIVE SERINE/ THREONINE PROTEIN KINASE
Species	*A. thaliana*	*Dunaliella tertiolecta*	*Antirrhinum majus* (Garden snapdragon)	*Medicago sativa* (Alfalfa)	*A. thaliana*
Identity %	70%	68%	70%	69%	69%
Similarity %	79%	76%	81%	79%	77%

TABLE 4

Degree of Amino Acid Identity and Similarity of PpPK-8 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	O82754	Q9M085	Q02779	Q05609	Q39886
Protein name	PUTATIVE SERINE/ THREONINE KINASE	PROTEIN KINASE-LIKE PROTEIN	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10	SERINE/ THREONINE-PROTEIN KINASE CTR1	PROTEIN KINASE
Species	*A. thaliana*	*A. thaliana*	*Homo sapiens* (Human)	*A. thaliana*	*Glycine max* (Soybean)
Identity %	25%	26%	27%	27%	26%
Similarity %	42%	40%	38%	40%	40%

TABLE 5

Degree of Amino Acid Identity and Similarity of PpPK-9 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9SL77	P34099	Q9TXB8	P40376	Q9SXP9
Protein name	PUTATIVE CAMP-DEPENDENT PROTEIN KINASE	CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT	SERINE/ THREO-NINE PROTEIN KINASE	CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT	CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT
Species	*A. thaliana*	*Dictyo-stelium discoideum* (Slime mold)	*Dictyo-stelium*	*Schizo-saccharomyces pombe* (Fission yeast)	*Euglena gracilis*
Identity %	45%	33%	32%	33%	28%
Similarity %	60%	48%	48%	50%	40%

TABLE 6

Degree of Amino Acid Identity and Similarity of PpCK-1 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9SZI1	Q9ZUP4	P42158	Q9LW62	Q39050
Protein name	COL-0 CASEIN KINASE I-LIKE PROTEIN	PUTATIVE CASEIN KINASE I	CASEIN KINASE I, DELTA ISOFORM LIKE	CASEIN KINASE	CASEIN KINASE I
Species	*A. thaliana.*	*A. thaliana*	*A. thaliana*	*A. thaliana*	*A. thaliana*
Identity %	49%	48%	48%	46%	40%
Similarity %	62%	61%	61%	58%	52%

TABLE 7

Degree of Amino Acid Identity and Similarity of PpCK-2 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9SZI1	P42158	Q9ZWB3	Q9ZUP4	Q9LSX4
Protein name	COL-0 CASEIN KINASE I-LIKE PROTEIN	CASEIN KINASE I	ADK1	PUTATIVE CASEIN KINASE I	CASEIN KINASE I

TABLE 7-continued

Degree of Amino Acid Identity and Similarity of PpCK-2 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9SZI1	P42158	Q9ZWB3	Q9ZUP4	Q9LSX4
Species	*A. thaliana.*	*A. thaliana*	*A. thaliana*	*A. thaliana*	*A. thaliana*
Identity %	64%	59%	60%	58%	57%
Similarity %	73%	66%	72%	67%	69%

TABLE 8

Degree of Amino Acid Identity and Similarity of PpCK-3 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	O64816	Q9ZR52	P28523	Q9SN18	Q08466
Protein name	PUTATIVE CASEIN KINASE II CATALYTIC SUBUNIT	CASEIN KINASE II ALPHA SUBUNIT	CASEIN KINASE II, ALPHA CHAIN	CASEIN KINASE II, ALPHA CHAIN 2 (CK II)	CASEIN KINASE II, ALPHA CHAIN 2
Species	*A. thaliana*	*Zea mays* (Maize)	*Z. mays*	*A. thaliana*	*A. thaliana*
Identity %	87%	89%	89%	88%	88%
Similarity %	93%	94%	93%	93%	93%

TABLE 9

Degree of Amino Acid Identity and Similarity of PpMPK-2 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9M136	Q40531	Q39024	Q40353	Q07176
Protein name	MAP KINASE 4	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF6	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK1
Species	*A. thaliana*	*Nicotiana tabacum* (Common tobacco)	*A. thaliana*	*M. sativa*	*M. sativa*
Identity %	70%	69%	69%	68%	66%
Similarity %	80%	78%	80%	79%	76%

TABLE 10

Degree of Amino Acid Identity and Similarity of PpMPK-3 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9SUX2	P13983	Q41192	O70495	Q9RLD9
Protein name	EXTENSIN-LIKE PROTEIN	EXTENSIN	NAPRP3	PLENTY-OF-PROLINES-101	FERULOYL-COA SYNTHETASE
Species	*A. thaliana*	*N. tabacum*	*Nicotiana alata* (Winged tobacco) (Persian tobacco)	*Mus musculus* (Mouse)	*Pseudomonas* sp.

TABLE 10-continued

Degree of Amino Acid Identity and Similarity of PpMPK-3 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9SUX2	P13983	Q41192	O70495	Q9RLD9
Identity %	12%	15%	22%	18%	11%
Similarity %	21%	22%	30%	26%	20%

TABLE 11

Degree of Amino Acid Identity and Similarity of PpMPK-4 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	O49975	O48616	Q9M6Q9	O80395	Q9S7U9
Protein name	PROTEIN KINASE ZMMEK1	MAP KINASE KINASE	MAP KINASE KINASE	MAP KINASE KINASE 2	MAP2K BETA PROTEIN
Species	*Z. mays*	*Lycopersicon esculentum* (Tomato)	*N. tabacum*	*A. thaliana*	*A. thaliana*
Identity %	59%	54%	53%	50%	50%

TABLE 12

Degree of Amino Acid Identity and Similarity of PpMPK-5 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	O49975	O48616	Q9M6Q9	O80395	Q9S7U9
Protein name	PROTEIN KINASE ZMMEK1	MAP KINASE KINASE	MAP KINASE KINASE	MAP KINASE KINASE 2	MAP2K BETA PROTEIN
Species	*Z. mays*	*L. esculentum*	*N. tabacum*	*A. thaliana*	*A. thaliana*
Identity %	59%	54%	53%	50%	50%
Similarity %	72%	66%	66%	62%	62%

TABLE 13

Degree of Amino Acid Identity and Similarity of PpCPK-1 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9SCS2	O04290	P53681	P93520	Q41792
Protein name	CDPK-RELATED PROTEIN KINASE	CDPK-RELATED PROTEIN KINASE	CDPK-RELATED PROTEIN KINASE	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE HOMOLOG	CDPK-RELATED PROTEIN KINASE

TABLE 13-continued

Degree of Amino Acid Identity and Similarity of PpCPK-1 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9SCS2	O04290	P53681	P93520	Q41792
Species	*A. thaliana*	*A. thaliana*	*Daucus carota* (Carrot)	*Z. mays*	*Z. mays*
Identity %	64%	64%	63%	63%	63%
Similarity %	76%	76%	75%	73%	74%

TABLE 14

Degree of Amino Acid Identity and Similarity of PpCPK-2 and Other Homologous Proteins GCG Gap program was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62)

	Swiss-Prot #				
	Q9S7Z4	Q42479	Q41790	O81390	Q9ZPM0
Protein name	CALCIUM-DEPENDENT PROTEIN KINASE	CALCIUM-DEPENDENT PROTEIN KINASE	CALCIUM-DEPENDENT PROTEIN KINASE	CALCIUM-DEPENDENT PROTEIN KINASE	CA2+-DEPENDENT PROTEIN KINASE
Species	*Marchantia polymorpha* (Liverwort)	*A. thaliana*	*Z. mays*	*N. tabacum*	*Mesembryanthemum crystallinum* (Common ice plant)
Identity %	66%	62%	59%	59%	59%
Similarity %	75%	73%	70%	68%	70%

Example 6

Cloning of the Full-Length *Physcomitrella Patens* cDNA Encoding for PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2

To isolate the clones encoding PK-6 (SEQ ID NO:14), PK-7 (SEQ ID NO:15), PK-8 (SEQ ID NO:16), PK-9 (SEQ ID NO:17), CK-1 (SEQ ID NO:18), CK-2 (SEQ ID NO:19), CK-3 (SEQ ID NO:20), MPK-2 (SEQ ID NO:21), MPK-3 (SEQ ID NO:22), MPK-4 (SEQ ID NO:23), MPK-5 (SEQ ID NO:24), CPK-1 (SEQ ID NO:25) and CPK-2 (SEQ ID NO:26) from *Physcomitrella patens*, cDNA libraries were created with SMART RACE cDNA Amplification kit (Clontech Laboratories) following manufacturer's instructions. Total RNA isolated as described in Example 3 was used as the template. The cultures were treated prior to RNA isolation as follows: Salt Stress: 2, 6, 12, 24, 48 hours with 1-M NaCl-supplemented medium; Cold Stress: 4° C. for the same time points as for salt; Drought Stress: cultures were incubated on dry filter paper for the same time points as for salt.

5' RACE Protocol

The EST sequences PK-6 (SEQ ID NO:1), PK-7 (SEQ ID NO:2), PK-8 (SEQ ID NO:3), PK-9 (SEQ ID NO:4), CK-1 (SEQ ID NO:5), CK-2 (SEQ ID NO:6), CK-3 (SEQ ID NO:7), MPK-2 (SEQ ID NO:8), MPK-3 (SEQ ID NO:9), MPK-4 (SEQ ID NO:10), MPK-5 (SEQ ID NO:11), CPK-1 (SEQ ID NO:12) and CPK-2 (SEQ ID NO:13) identified from the database search as described in Example 4 were used to design oligos for RACE (see Table 15). The extended sequences for these genes were obtained by performing Rapid Amplification of cDNA Ends polymerase chain reaction (RACE PCR) using the Advantage 2 PCR kit (Clontech Laboratories) and the SMART RACE cDNA amplification kit (Clontech Laboratories) using a Biometra T3 Thermocycler following the manufacturer's instructions. The sequences obtained from the RACE reactions corresponded to full-length coding regions of CC-2 and CC-3 and were used to design oligos for full-length cloning of the respective genes (see below full-length amplification).

Full-Length Amplification

Full-length clones corresponding PK-6 (SEQ ID NO:14), PK-7 (SEQ ID NO:15), PK-8 (SEQ ID NO:16), PK-9 (SEQ ID NO:17), CK-1 (SEQ ID NO:18), CK-2 (SEQ ID NO:19), CK-3 (SEQ ID NO:20), MPK-2 (SEQ ID NO:21), MPK-3 (SEQ ID NO:22), MPK-4 (SEQ ID NO:23), MPK-5 (SEQ ID NO:24), CPK-1 (SEQ ID NO:25) and CPK-2 (SEQ ID NO:26) were obtained by performing polymerase chain reaction (PCR) with gene-specific primers (see Table 15) and the original EST as the template. The conditions for the reaction were standard conditions with PWO DNA polymerase (Roche). PCR was performed according to standard conditions and to manufacturer's protocols (Sambrook et al., 1989 Molecular Cloning, A Laboratory Manual. 2nd Edition. Cold Spring Harbor Laboratory Press. Cold Spring Harbor, N.Y., Biometra T3 Thermocycler). The parameters for the reaction were: five minutes at 94° C. followed by five cycles of one minute at 94° C., one minute at 50° C. and 1.5 minutes at 72° C. This was followed by twenty five cycles of one minute at 94° C., one minute at 65° C. and 1.5 minutes at 72° C.

The amplified fragments were extracted from agarose gel with a QIAquick Gel Extraction Kit (Qiagen) and ligated into the TOPO pCR 2.1 vector (Invitrogen) following manufacturer's instructions. Recombinant vectors were transformed into Top10 cells (Invitrogen) using standard conditions (Sambrook et al. 1989. Molecular Cloning, A Laboratory Manual. 2nd Edition. Cold Spring Harbor Laboratory Press. Cold Spring Harbor, N.Y.). Transformed cells were selected for on

LB agar containing 100 μg/ml carbenicillin, 0.8 mg X-gal (5-bmmo-4-chloro-3-indolyl-β-D-galactoside) and 0.8 mg IPTG (isopropylthio-β-D-galactoside) grown overnight at 37° C. White colonies were selected and used to inoculate 3 ml of liquid LB containing 100 μg/ml ampicillin and grown overnight at 37° C. Plasmid DNA was extracted using the QIAprep Spin Miniprep Kit (Qiagen) following manufacturer's instructions. Analyses of subsequent clones and restriction mapping was performed according to standard molecular biology techniques (Sambrook et al., 1989 Molecular Cloning, A Laboratory Manual. 2nd Edition. Cold Spring Harbor Laboratory Press. Cold Spring Harbor, N.Y.).

TABLE 15

Scheme and primers used for cloning of full-length clones

Gene	Final product Sites	Isolation Method	Primers Race	Primers RT-PCR
PpPK-6	XmaI/HpaI	5' RACE and RT-PCR for Full-length clone	RC782: (SEQ ID NO: 43) CCACGGTCTTCGGC TGCTGGTCGTG RC783: (SEQ ID NO: 44) GCAGCACAGCACC ACCAGCGGCTAT NVT: (SEQ ID NO: 45) GCGCCCAGTGAGTA GCTCCAGCATT	RC858: (SEQ ID NO: 46) ATCCCGGGTGAGTA TCACTTACGGTGGC GA RC859: (SEQ ID NO: 47) GCGTTAACTCGACC AAGGTCACTATTCC AAGCA
PpPK-7	XmaI/HpaI	5' RACE and RT-PCR for Full-length clone	RC250: (SEQ ID NO: 48) CGGTGCCCACCTCG TTCCTGTGGTT	RC590: (SEQ ID NO: 49) ATCCCGGGAGTGGG TGGTTGGACTGTAA GGA RC591: (SEQ ID NO: 50) GCGTTAACCTTCGTC TTGGACAGGTAGAG GTTAC
PpPK-8	XmaI/HpaI	5' RACE and RT-PCR for Full-length clone	(SEQ ID NO: 51) GACTCAGCCCCGTA ATCCTTCAACA	RC1016: (SEQ ID NO: 52) ATCCCGGGCAACGA GAAGCATTCGAGAT GGC RC1021: (SEQ ID NO: 53) GCGTTAACGAGCAT CACGATACTCGGTG ATTTC
PpPK-9	XmaI/SacI	5' RACE and RT-PCR for Full-length clone	RC263: (SEQ ID NO: 54) CGACGGCTAATACC ACGTTGGCGACCA	RC831: (SEQ ID NO: 55) ATCCCGGGCTGTGA TGTCGGTGTGGTGCT CTGC RC832: (SEQ ID NO: 56) GCGAGCTCGCACCA CTGAATGATGGAGA CTCAGG
PpCK-1	XmaI/HpaI	5' RACE and RT-PCR for Full-length clone	NVT: (SEQ ID NO: 57) CGACCGCAGCCCAT GAGGAAGTTAT	RC614: (SEQ ID NO: 58) ATCCCGGGCTCACG TAGTGCACTGAACT CTGTC RC615: (SEQ ID NO: 59) GCGTTAACATGCCC ATCTTCTCATACTCA GACC

TABLE 15-continued

Scheme and primers used for cloning of full-length clones

Gene	Final product Sites	Isolation Method	Primers Race	Primers RT-PCR
PpCK-2	XmaI/HpaI	5' RACE and RT-PCR for Full-length clone	NVT: (SEQ ID NO: 60) CTCGCCTACCAAGC CCCATTAGAAA	RC1012: (SEQ ID NO: 61) ATCCCGGGTTGTCG AGGACGGAGAGAGA AGAG RC1015: (SEQ ID NO: 62) GCGTTAACCTTAGG AATCGTATGGCAGA GAGCT
PpCK-3	HpaI/SacI	5' RACE and RT-PCR for Full-length clone	NVT: (SEQ ID NO: 63) GCTTCACAATGTTG GGCCCTCCACA	RC640: (SEQ ID NO: 64) GCGTTAACGGGAGG AAGGTCGGGGGAAG AGACG RC641: (SEQ ID NO: 65) GCGAGCTCAGCGCT TCGCACAACTGAGA AACCT
PpMPK-2	XmaI/HpaI	5' RACE and RT-PCR for Full-length clone	NVT: (SEQ ID NO: 66) ACGAGAAGGTTGGT GGGCTTCAAGT	RC664: (SEQ ID NO: 67) ATCCCGGGCGAGCC ATGGCGCCACTTGCT T RC665: (SEQ ID NO: 68) GCGTTAACGCCGAG CAACAATGTCTGCT GGATG
PpMPK-3	XmaI/HpaI	5' RACE and RT-PCR for Full-length clone	RC268: (SEQ ID NO: 69) CCCGGTAAGCCATC GGAGTGTGGAA	RC662: (SEQ ID NO: 70) ATCCCGGGCTTGTAT TGGCTCGGATAATTT RC663: (SEQ ID NO: 71) GCGTTAACGGCAAT ATCTGCACAGCCGTT CACT
PpMPK-4	XmaI/SacI	5' RACE and RT-PCR for Full-length clone	NVT: (SEQ ID NO: 72) GTGTCTCGCTGGGC CAAGGAATGAA	RC1001: (SEQ ID NO: 73) ATCCCGGGCGGTCG AGTCGTATTAGGTG TTGTTTC RC1005: (SEQ ID NO: 74) GAGCTCCGGTAGGT CCGACCTCTTCAATT G
PpMPK-5	XmaI/SacI	5' RACE and RT-PCR for Full-length clone	RC266: (SEQ ID NO: 75) GACGACGCGAAGC CCGGTGTGGTTGA	RC572: (SEQ ID NO: 76) ATCCCGGGAGAGGC TGATCTGATGCTACA GT RC573: (SEQ ID NO: 77) ATGAGCTCTGGCGG ATTGGCGAGGTAGT TCGAC

TABLE 15-continued

Scheme and primers used for cloning of full-length clones

Gene	Final product Sites	Isolation Method	Primers Race	Primers RT-PCR
pCPK-1	XmaI/HpaI	5' RACE and RT-PCR for Full-length clone	RC526: (SEQ ID NO: 78) CGGCGCAACGTAGT ATGCGCTTCCA RC723N: (SEQ ID NO: 79) CGCGGTGAACAAC ACCTTGCAGGTGAC RC767: (SEQ ID NO: 80) GCTCGGGTCAGCCC TCAACACCGCA NVT: (SEQ ID NO: 81) GTTAAAGCTTGTGC AGCAGTCATGC	RC817: (SEQ ID NO: 82) ATCCCGGGTGTAGG CGGGCGAGGTTCGA TGC RC818: (SEQ ID NO: 83) GCGTTAACGACAAC CGGAGTAGAACGGC AGTCCA
pCPK-2	XmaI/HpaI	5' RACE and RT-PCR for Full-length clone	NVT: (SEQ ID NO: 84) AGAAGCGAGGAAT GGGCAGGGACGA	RC703: (SEQ ID NO: 85) ATCCCGGGCGAACT GCGATCTGAGATTC CAAC RC704: (SEQ ID NO: 86) GCGTTAACGAGATC CAACCGAAGCCATC CTACGA

Example 7

Engineering Stress-Tolerant *Arabidopsis* Plants by Over-Expressing the Genes PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2 Binary Vector Construction: Kanamycin

The plasmid construct pACGH101 was digested with PstI (Roche) and FseI (NEB) according to manufacturers' instructions. The fragment was purified by agarose gel and extracted via the Qiaex II DNA Extraction kit (Qiagen). This resulted in a vector fragment with the *Arabidopsis* Actin2 promoter with internal intron and the OCS3 terminator. Primers for PCR amplification of the NPTII gene were designed as follows:

5'NPT-Pst:
(SEQ ID NO: 87)
GCG-CTG-CAG-ATT-TCA-TTT-GGA-GAG-GAC-ACG

3'NPT-Fse:
(SEQ ID NO: 88)
CGC-GGC-CGG-CCT-CAG-AAG-AAC-TCG-TCA-AGA-AGG-CG.

The 0.9 kilobase NPTII gene was amplified via PCR from pCambia 2301 plasmid DNA [94° C. 60 sec, {94° C. 60 sec, 61° C. (−0.1° C. per cycle) 60 sec, 72° C. 2 min}×25 cycles, 72° C. 10 min on Biometra T-Gradient machine], and purified via the Qiaquick PCR Extraction kit (Qiagen) as per manufacturer's instructions. The PCR DNA was then subcloned into the pCR-BluntII TOPO vector (Invitrogen) pursuant to the manufacturer's instructions (NPT-Topo construct). These ligations were transformed into Top 10 cells (Invitrogen) and grown on LB plates with 50 ug/ml kanamycin sulfate overnight at 37° C. Colonies were then used to inoculate 2 ml LB media with 50 ug/ml kanamycin sulfate and grown overnight at 37° C. Plasmid DNA was recovered using the Qiaprep Spin Miniprep kit (Qiagen) and sequenced in both the 5' and 3' directions using standard conditions. Subsequent analysis of the sequence data using VectorNTI software revealed no PCR errors present in the NPTII gene sequence.

The NPT-Topo construct was then digested with PstI (Roche) and FseI (NEB) according to manufacturers' instructions. The 0.9 kilobase fragment was purified on agarose gel and extracted by Qiaex II DNA Extraction kit (Qiagen), The Pst/Fse insert fragment from NPT-Topo and the Pst/Fse vector fragment from pACGH101 were then ligated together using T4 DNA Ligase (Roche) following manufacturer's instructions. The ligation was then transformed into Top10 cells (Invitrogen) under standard conditions, creating pBPSsc019 construct. Colonies were selected on LB plates with 50 ug/ml kanamycin sulfate and grown overnight at 37° C. These colonies were then used to inoculate 2 ml LB media with 50 ug/ml kanamycin sulfate and grown overnight at 37° C. Plasmid DNA was recovered using the Qiaprep Spin Miniprep kit (Qiagen) following the manufacturer's instructions.

The pBPSSC019 construct was digested with KpnI and BsaI (Roche) according to manufacturer's instructions. The fragment was purified via agarose gel and then extracted via the Qiaex II DNA Extraction kit (Qiagen) as per its instructions, resulting in a 3 kilobase Act-NPT cassette, which included the *Arabidopsis* Acting promoter with internal intron, the NPTII gene and the OCS3 terminator.

The pBPSJH001 vector was digested with SpeI and ApaI (Roche) and blunt-end filled with Klenow enzyme and 0.1 mM dNTPs (Roche) according to manufacture's instructions. This produced a 10.1 kilobase vector fragment minus the Gentamycin cassette, which was recircularized by self-ligating with T4 DNA Ligase (Roche), and transformed into Top10 cells (Invitrogen) via standard conditions. Transformed cells were selected for on LB agar containing 50 μg/ml kanmycin sulfate and grown overnight at 37° C. Colonies were then used to inoculate 2 ml of liquid LB containing 50 μg/ml kanamycin sulfate and grown overnight at 37° C. Plasmid DNA was extracted using the QIAprep Spin Mini-

prep Kit (Qiagen) following manufacture's instructions. The recircularized plasmid was then digested with KpnI (Roche) and extracted from agarose gel via the Qiaex II DNA Extraction kit (Qiagen) as per manufacturer's instructions.

The Act-NPT Kpn-cut insert and the Kpn-cut pBPSJH001 recircularized vector were then ligated together using T4 DNA Ligase (Roche) and transformed into Top10 cells (Invitrogen) as per manufacturers' instructions. The resulting construct, pBPSsc022, now contained the Super Promoter, the GUS gene, the NOS terminator, and the Act-NPT cassette. Transformed cells were selected for on LB agar containing 50 μg/ml kanmycin sulfate and grown overnight at 37° C. Colonies were then used to inoculate 2 ml of liquid LB containing 50 μg/ml kanamycin sulfate and grown overnight at 37° C. Plasmid DNA was extracted using the QIAprep Spin Miniprep Kit (Qiagen) following manufacturer's instructions. After confirmation of ligation success via restriction digests, pBPSsc022 plasmid DNA was further propigated and recovered using the Plasmid Midiprep Kit (Qiagen) following the manufacturer's instructions.

Subeloning of PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2 into the Binary Vector

The fragments containing the different *Physcomitrella patens* protein kinases were subcloned from the recombinant PCR2.1 TOPO vectors by double digestion with restriction enzymes (see Table 16) according to manufacturer's instructions. The subsequence fragment was excised from agarose gel with a QIAquick Gel Extraction Kit (QIAgen) according to manufacture's instructions and ligated into the binary vectors pGMSG, cleaved with XmaI and Ecl136II and dephosphorylated prior to ligation. The resulting recombinant pGMSG contained the corresponding transcription factor in the sense orientation under the constitutive super promoter.

TABLE 16

Listed are the names of the various constructs of the *Physcomitrella patens* transcription factors used for plant transformation

Gene	Enzymes used to generate gene fragment	Enzymes used to restrict pBPSJH001	Binary Vector Construct
PpPK-6	XmaI/HpaI	XmaI/SacI	pBPSJyw022
PpPK-7	XmaI/HpaI	XmaI/Ecl136	pBPSJyw012
PpPK-8	XmaI/HpaI	XmaI/Ecl136	pBPSJYW030
PpPK-9	XmaI/SacI	XmaI/SacI	PBPSERG010
PpCK-1	XmaI/HpaI	XmaI/Ecl136	pBPSSY012
PpCK-2	XmaI/HpaI	XmaI/Ecl136	pBPSJyw034
PpCK-3	HpaI/SacI	SmaI/SacI	pBPSSY011
PpMPK-2	XmaI/HpaI	XmaI/Ecl136	pBPSSY016
PpMPK-3	XmaI/HpaI	XmaI/Ecl136	pBPSJyw014
PpMPK-4	XmaI/SacI	XmaI/SacI	pBPSJyw025
PpMPK-5	XmaI/SacI	XmaI/SacI	PBPSERG009
PpCPK-1	XmaI/HpaI	XmaI/Ecl136	PBPSERG019
PpCPK-2	XmaI/HpaI	XmaI/Ecl136	pBPSJyw008

Agrobacterium Transformation

The recombinant vectors were transformed into *Agrobacterium tumefaciens* C58C1 and PMP90 according to standard conditions (Hoefgen and Willmitzer, 1990).

Plant Transformation

Arabidopsis thaliana ecotype C24 were grown and transformed according to standard conditions (Bechtold 1993, Acad. Sci. Paris. 316:1194-1199; Bent et al. 1994, Science 265:1856-1860).

Screening of Transformed Plants

T1 seeds were sterilized according to standard protocols (Xiong et al. 1999, Plant Molecular Biology Reporter 17: 159-170). Seeds were plated on ½ Murashige and Skoog media (MS) (Sigma-Aldrich) pH 5.7 with KOH, 0.6% agar and supplemented with 1% sucrose, 0.5 g/L 2-[N-Morpholino]ethansulfonic acid (MES) (Sigma-Aldrich), 50 μg/ml kanamycin (Sigma-Aldrich), 500 μg/ml earbenicillan (Sigma-Aldrich) and 2 μg/ml benomyl (Sigma-Aldrich). Seeds on plates were vernalized for four days at 4° C. The seeds were germinated in a climatic chamber at an air temperature of 22° C. and light intensity of 40 micromol s^{-1} m^{-2} (white light; Philips TL 65W/25 fluorescent tube) and 16 hours light and 8 hours dark day length cycle. Transformed seedlings were selected after 14 days and transferred to ½ MS media pH 5.7 with KOH 0.6% agar plates supplemented with 0.6% agar, 1% sucrose, 0.5 g/L MES (Sigma-Aldrich), and 2 μg/ml benomyl (Sigma-Aldrich) and allowed to recover for five-seven days.

Drought Tolerance Screening

T1 seedlings were transferred to dry, sterile filter paper in a petri dish and allowed to desiccate for two hours at 80% RH (relative humidity) in a Percieval Growth Cabinet MLR-350H, micromole s^{-1} m^{-2} (white light; Philips TL 65W/25 fluorescent tube). The RH was then decreased to 60% and the seedlings were desiccated further for eight hours. Seedlings were then removed and placed on ½ MS 0.6% agar plates supplemented with 2 μg/ml benomyl (Sigma-Aldrich) and 0.5 g/L MES (Sigma-Aldrich) and scored after five days.

Under drought stress conditions, PpPK-6 over-expressing *Arabidopsis thaliana* plants showed a 95% (20 survivors from 21 stressed plants) survival rate to the stress screening; PpPK-8, 40% (2 survivors from 5 stressed plants), PpPK-9, 78% (38 survivors from 49 stressed plants), PpCK-1, 50% (5 survivors from 10 stressed plants), PpCK-2, 52% (16 survivors from 31 stressed plants), PpCK-3, 60% (3 survivors from 5 stressed plants), PpMPK-2, 100% (52 survivors from 52 stressed plants), PpMPK-3, 98% (44 survivors from 45 stressed plants), PpMPK-4, 92% (11 survivors from 12 stressed plants), PpMPK-5, 100% (9 survivors from 9 stressed plants), PpCPK-1, 60% (12 survivors from 20 stressed plants), PpCPK-2, 89% (17 survivors from 19 stressed plants), whereas the untransformed control only showed an 11% survival rate (1 survivor from 9 stressed plants). It is noteworthy that the analyses of these transgenic lines were performed with T1 plants, and therefore, the results will be better when a homozygous, strong expresser is found.

TABLE 17

Summary of the drought stress tests

	Drought Stress Test		
Gene Name	Number of survivors	Total number of plants	Percentage of survivors
PpPK-6	20	21	95%
PpPK-8	2	5	40%
PpPK-9	38	49	78%
PpCK-1	5	10	50%
PpCK-2	16	31	52%
PpCK-3	3	5	60%
PpMPK-2	52	52	100%
PpMPK-3	44	45	98%
PpMPK-4	11	12	92%
PpMPK-5	9	9	100%

Freezing Tolerance Screening

Seedlings were moved to petri dishes containing ½ MS 0.6% agar supplemented with 2% sucrose and 2 μg/ml benomyl. After four days, the seedlings were incubated at 4° C. for 1 hour and then covered with shaved ice. The seedlings

were then placed in an Environmental Specialist ES2000 Environmental Chamber and incubated for 3.5 hours beginning at −1.0° C. decreasing 1° C./ hour. The seedlings were then incubated at −5.0° C. for 24 hours and then allowed to thaw at 5° C. for 12 hours. The water was poured off and the seedlings were scored after 5 days.

Under freezing stress conditions, PpPK-7 over-expressing *Arabidopsis thaliana* plants showed a 73% (8 survivors from 11 stressed plants) survival rate to the stress screening; PpPK-9, 100% (45 survivors from 45 stressed plants), PpCK-1, 100% (14 survivors from 14 stressed plants), PpMPK-2, 68% (36 survivors from 53 stressed plants), PpMPK-3, 92% (24 survivors from 26 stressed plants), PpCPK-2, 64% (7 survivors from 11 stressed plants), whereas the untransformed control only showed a 2% survival rate (1 survivor from 48 stressed plants). It is noteworthy that the analyses of these transgenic lines were performed with T1 plants, and therefore, the results will be better when a homozygous, strong expresser is found.

TABLE 18

Summary of the freezing stress tests

	Freezing Stress Test		
Gene Name	Number of survivors	Total number of plants	Percentage of survivors
PpPK-7	8	11	73%
PpPK-9	45	45	100%
PpCK-1	14	14	100%
PpMPK-2	36	53	68%
PpMPK-3	24	26	92%
PpCPK-2	7	11	64%
Control	1	48	2%

Salt Tolerance Screening

Seedlings were transferred to filter paper soaked in ½ MS and placed on ½ MS 0.6% agar supplemented with 2 μg/ml benomyl the night before the salt tolerance screening. For the salt tolerance screening, the filter paper with the seedlings was moved to stacks of sterile filter paper, soaked in 50 mM NaCl, in a petri dish. After two hours, the filter paper with the seedlings was moved to stacks of sterile filter paper, soaked with 200 mM NaCl, in a petri dish. After two hours, the filter paper with the seedlings was moved to stacks of sterile filter paper, soaked in 600 mM NaCl, in a petri dish. After 10 hours, the seedlings were moved to petri dishes containing ½ MS 0.6% agar supplemented with 2 μg/ml benomyl. The seedlings were scored after 5 days.

The transgenic plants are screened for their improved salt tolerance demonstrating that transgene expression confers salt tolerance.

Example 8

Detection of the PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2 Transgenes in the Transgenic *Arabidopsis* Lines

One leaf from a wild type and a transgenic *Arabidopsis* plant was homogenized in 250 μl Hexadecyltrimethyl ammonium bromide (CTAB) buffer (2% CTAB, 1.4 M NaCl, 8 mM EDTA and 20 mM Tris pH 8.0) and 1 μl β-mercaptoethanol. The samples were incubated at 60-65° C. for 30 minutes and 250 μl of Chloroform was then added to each sample. The samples were vortexed for 3 minutes and centrifuged for 5 minutes at 18,000×g. The supernatant was taken from each sample and 150 μl isopropanol was added. The samples were incubated at room temperature for 15 minutes, and centrifuged for 10 minutes at 18,000×g. Each pellet was washed with 70% ethanol, dried, and resuspended in 20 μl TE. 4 μl of above suspension was used in a 20 μl PCR reaction using Taq DNA polymerase (Roche Molecular Biochemicals) according to the manufacturer's instructions.

Binary vector plasmid with each gene cloned in was used as positive control, and the wild-type C24 genomic DNA was used as negative control in the PCR reactions. 10 μl PCR reaction was analyzed on 0.8% agarose-ethidium bromide gel.

PpPk-6: The primers used in the reactions are:

```
GCTGACACGCCAAGCCTCGCTAGTC          (SEQ ID NO: 89)

GCGTTAACTCGACCAAGGTCACTATTCCAAGCA (SEQ ID NO: 90)
```

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 2.8 kb fragment was produced from the positive control and the transgenic plants.

PpPk-7: The primers used in the reactions are:

```
                                   (SEQ ID NO: 89)
GCTGACACGCCAAGCCTCGCTAGTC

                                   (SEQ ID NO: 91)
GCGTTAACCTTCGTCTTGGACAGGTAGAGGTTAC
```

The primers were used in the first round of reactions with the following program: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 1.1 kb fragment was generated from the positive control and the T1 transgenic plants.

PpPK-8: The primers used in the reactions were:

```
GCTGACACGCCAAGCCTCGCTAGTC          (SEQ ID NO: 89)

GCGTTAACGAGCATCACGATACTCGGTGATTTC (SEQ ID NO: 92)
```

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 1.6 kb fragment was produced from the positive control and the transgenic plants.

PpPK-9: The primers used in the reactions are:

```
                                   (SEQ ID NO: 89)
GCTGACACGCCAAGCCTCGCTAGTC

                                   (SEQ ID NO: 93)
GCGAGCTCGCACCACTGAATGATGGAGACTCAGG
```

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 1.4 kb fragment was produced from the positive control and the transgenic plants.

PpCK-1: The primers used in the reactions are:

```
                                   (SEQ ID NO: 89)
GCTGACACGCCAAGCCTCGCTAGTC

                                   (SEQ ID NO: 94)
GCGTTAACATGCCCATCTTCTCATACTCAGACC
```

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 1.7 kb fragment was produced from the positive control and the transgenic plants.

PpCK-2: The primers used in the reactions are:

GCTGACACGCCAAGCCTCGCTAGTC (SEQ ID NO: 89)

GCGTTAACCTTAGGAATCGTATGGCAGAGAGCT (SEQ ID NO: 95)

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 1.9 kb fragment was produced from the positive control and the transgenic plants.

PpCK-3: The primers used in the reactions are:

GCTGACACGCCAAGCCTCGCTAGTC (SEQ ID NO: 89)

GCGAGCTCAGCGCTTCGCACAACTGAGAAACCT (SEQ ID NO: 96)

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 1.2 kb fragment was produced from the positive control and the transgenic plants.

PpMPK-2: The primers used in the reactions are:

GCTGACACGCCAAGCCTCGCTAGTC (SEQ ID NO: 89)

GCGTTAACGGCAATATCTGCACAGCCGTTCACT (SEQ ID NO: 97)

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 1.7 kb fragment was produced from the positive control and the transgenic plants.

PpMPK-3: The primers used in the reactions are:

GCTGACACGCCAAGCCTCGCTAGTC (SEQ ID NO: 89)

GCGTTAACGGCAATATCTGCACAGCCGTTCACT (SEQ ID NO: 98)

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 2.2 kb fragment was produced from the positive control and the transgenic plants.

PpMPK-4: The primers used in the reactions are:

GCTGACACGCCAAGCCTCGCTAGTC (SEQ ID NO: 89)

GAGCTCCGGTAGGTCCGACCTCTTCAATTG (SEQ ID NO: 99)

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 1.7 kb fragment was produced from the positive control and the transgenic plants.

PpMPK-5: The primers used in the reactions are:

GCTGACACGCCAAGCCTCGCTAGTC (SEQ ID NO: 89)

ATGAGCTCTGGCGGATTGGCGAGGTAGTTCGAC (SEQ ID NO: 100)

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 1.4 kb fragment was produced from the positive control and the transgenic plants.

PpCPK-1: The primers used in the reactions are:

GCTGACACGCCAAGCCTCGCTAGTC (SEQ ID NO: 89)

GCGTTAACGACAACCGGAGTAGAACGGCAGTCCA (SEQ ID NO: 101)

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 2.3 kb fragment was produced from the positive control and the transgenic plants.

PpCPK-2: The primers used in the reactions are:

GCTGACACGCCAAGCCTCGCTAGTC (SEQ ID NO: 89)

GCGTTAACGAGATCCAACCGAAGCCATCCTACGA (SEQ ID NO: 102)

The PCR program was as following: 30 cycles of 1 minute at 94° C., 1 minute at 62° C. and 4 minutes at 72° C., followed by 10 minutes at 72° C. A 2.2 kb fragment was produced from the positive control and the transgenic plants.

The transgenes were successfully amplified from the T1 transgenic lines, but not from the wild type C24. This result indicates that the T1 transgenic plants contain at least one copy of the transgenes. There was no indication of existence of either identical or very similar genes in the untransformed *Arabidopsis thaliana* control which could be amplified by this method.

Example 9

Detection of the PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2 Transgene mRNA in Transgenic *Arabidopsis* Lines

Transgene expression was detected using RT-PCR. Total RNA was isolated from stress-treated plants using a procedure adapted from (Verwoerd et al., 1989 NAR 17:2362). Leaf samples (50-100 mg) were collected and ground to a fine powder in liquid nitrogen. Ground tissue was resuspended in 500 μl of a 80° C., 1:1 mixture, of phenol to extraction buffer (100 mM LiCl, 100 mM Tris p18, 10 mM EDTA, 1% SDS), followed by brief vortexing to mix. After the addition of 250 μl of chloroform, each sample was vortexed briefly. Samples were then centrifuged for 5 minutes at 12,000×g. The upper aqueous phase was removed to a fresh eppendorf tube. RNA was precipitated by adding $^1/_{10}{}^{th}$ volume 3M sodium acetate and 2 volumes 95% ethanol. Samples were mixed by inversion and placed on ice for 30 minutes. RNA was pelleted by centrifugation at 12,000×g for 10 minutes. The supernatant was removed and pellets briefly air-dried. RNA sample pellets were resuspended in 10 μl DEPC treated water. To remove contaminating DNA from the samples, each was treated with RNase-free DNase (Roche) according to the manufacturer's recommendations. cDNA was synthesized from total RNA using the 1st Strand cDNA synthesis kit (Boehringer Mannheim) following manufacturer's recommendations.

PCR amplification of a gene-specific fragment from the synthesized cDNA was performed using Tag DNA polymerase (Roche) and gene-specific primers (see Table 15 for primers) in the following reaction: 1× PCR buffer, 1.5 mM $MgCl_2$, 0.2 μM each primer, 0.2 μM dNTPs, 1 unit polymerase, 5 μl cDNA from synthesis reaction. Amplification was performed under the following conditions: Denaturation, 95° C., 1 minute; annealing, 62° C., 30 seconds; extension, 72° C., 1 minute, 35 cycles; extension, 72° C., 5 minutes; hold, 4° C., forever. PCR products were run on a 1% agarose

gel, stained with ethidium bromide, and visualized under UV light using the Quantity-One gel documentation system (Bio-Rad).

Expression of the transgenes was detected in the T1 transgenic line. This result indicated that the transgenes are expressed in the transgenic lines and strongly suggested that their gene product improved plant stress tolerance in the transgenic line. On the other hand, no expression of identical or very similar endogenous genes could be detected by this method. These results are in agreement with the data from Example 7. This greatly supports our statement that the observed stress tolerance is due to the introduced transgene.

PpPK-6

(SEQ ID NO: 103)
CCCAGTAATAGCAGGGTTGGAGGAA

(SEQ ID NO: 104)
GGCTGCCTGAAGATCCGCTACAGAG

PpPK-7

(SEQ ID NO: 105)
CGTCAGGCTACTTTGCGTGGAGCAC

(SEQ ID NO: 106)
CGGTGCTGGCTAACACCAGGCCAGA

PpPK-8

(SEQ ID NO: 107)
ATCCCGGGCAACGAGAAGCATTCGAGATGGC

(SEQ ID NO: 108)
GCGTTAACGAGCATCACGATACTCGGTGATTTC

PpPK-9

(SEQ ID NO: 109)
CGTGGCATCTCTCCCGATGTTCTTA

(SEQ ID NO: 110)
GGCCAACTGAAGGCGTGTCATGATC

PpCK-1

(SEQ ID NO: 111)
CTCGAGGGCTCGTTCACCGTGACCT

(SEQ ID NO: 112)
CGGAGGTAACAGTAGTCAGGCTGCTC

PpCK-2

(SEQ ID NO: 113)
CCGCGACCCTTCCACGCATCAGCAT

(SEQ ID NO: 114)
CCTCCAGGAAGCCTGCGCCGAGAAG

PpCK-3

(SEQ ID NO: 115)
GGACATTGTCCGTGATCAGCAATCGA

(SEQ ID NO: 116)
CAGCCTCTGGAACAACCAGACGCTG

PpMPK-2

(SEQ ID NO: 117)
GTCACCGCGAGGTACAAGCCACCAC

(SEQ ID NO: 118)
GCAGCTCTGGAGCTCTGTACCACCT

PpMPK-3

(SEQ ID NO: 119)
ACGGCCACGTCGAGAATCTGAGCAA

(SEQ ID NO: 120)
CGAAGTGCTCGCAAGCAATGCCGAA

-continued

PpMPK-4

(SEQ ID NO: 121)
ATCCCGGGCGGTCGAGTCGTATTAGGTGTTGTTTC

(SEQ ID NO: 122)
GAGCTCCGGTAGGTCCGACCTCTTCAATTG

PpMPK-5

(SEQ ID NO: 123)
GGGCAACTGTCAATAGCAGACCTGGA

(SEQ ID NO: 124)
GCAAGTCCCAACGAACGTGTCTCGCT

PpCPK-1

(SEQ ID NO: 125)
GCGAAGATGACGACTGCTATTGCGA

(SEQ ID NO: 126)
CGTGATGACTCCAATGCTCCATACG

PpCPK-2

(SEQ ID NO: 127)
GCCAGCATCGAGGTCAGTATCCGGTGT

(SEQ ID NO: 128)
GTCTGTGGCCTTCAGAGGCGCATCCTC

Amplification was performed under the following conditions: Denaturation, 95° C., 1 minute; annealing, 62° C., 30 seconds; extension, 72° C., 1 minute, 35 cycles; extension, 72° C., 5 minutes; hold, 4° C., forever. PCR products were run on a 1% agarose gel, stained with ethidium bromide, and visualized under UV light using the Quantity-One gel documentation system (Bio-Rad).

Expression of the transgenes was detected in the T1 transgenic line. These results indicated that the transgenes are expressed in the transgenic lines and strongly suggested that their gene product improved plant stress tolerance in the transgenic lines. In agreement with the previous statement, no expression of identical or very similar endogenous genes could be detected by this method. These results are in agreement with the data from Example 7.

Example 10

Engineering Stress-Tolerant Soybean Plants by Over-Expressing the PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2 Gene

The constructs pBPSJyw022, pBPSJyw012, pBPSJYW030, PBPSERG010, pBPSSY012, pBPSJyw034, pBPSSY011, pBPSSY016, pBPSJyw014, pBPSJyw025, PBPSERG009, PBPSERG019 and pBPSJyw008 are used to transform soybean as described below.

Seeds of soybean are surface sterilized with 70% ethanol for 4 minutes at room temperature with continuous shaking, followed by 20% (v/v) Clorox supplemented with 0.05% (v/v) Tween for 20 minutes with continuous shaking. Then, the seeds are rinsed 4 times with distilled water and placed on moistened sterile filter paper in a Petri dish at room temperature for 6 to 39 hours. The seed coats are peeled off, and cotyledons are detached from the embryo axis. The embryo axis is examined to make sure that the meristematic region is not damaged. The excised embryo axes are collected in a half-open sterile Petri dish and air-dried to a moisture content less than 20% (fresh weight) in a sealed Petri dish until further use.

Agrobacterium tumefaciens culture is prepared from a single colony in LB solid medium plus appropriate antibiotics (e.g, 100 mg/l streptomycin, 50 mg/l kanamycin) followed by growth of the single colony in liquid LB medium to an optical

density at 600 nm of 0.8. Then, the bacteria culture is pelleted at 7000 rpm for 7 minutes at room temperature, and resuspended in MS (Murashige and Skoog, 1962) medium supplemented with 100 μM acetosyringone. Bacteria cultures are incubated in this pre-induction medium for 2 hours at room temperature before use. The axis of soybean zygotic seed embryos at approximately 15% moisture content are imbibed for 2 hours at room temperature with the pre-induced *Agrobacterium* suspension culture. The embryos are removed from the imbibition culture and are transferred to Petri dishes containing solid MS medium supplemented with 2% sucrose and incubated for 2 days, in the dark at room temperature. Alternatively, the embryos are placed on top of moistened (liquid MS medium) sterile filter paper in a Petri dish and incubated under the same conditions described above. After this period, the embryos are transferred to either solid or liquid MS medium supplemented with 500 mg/L carbenicillin or 300 mg/L cefotaxime to kill the *agrobacteria*. The liquid medium is used to moisten the sterile filter paper. The embryos are incubated during 4 weeks at 25° C., under 150 μmol $m^{-2}sec^{-1}$ and 12 hours photoperiod. Once the seedlings produce roots, they are transferred to sterile metromix soil. The medium of the in vitro plants is washed off before transferring the plants to soil. The plants are kept under a plastic cover for 1 week to favor the acclimatization process. Then the plants are transferred to a growth room where they are incubated at 25° C., under 150 μmol $m^{-2}sec^{-1}$ light intensity and 12 hours photoperiod for about 80 clays,

The transgenic plants are then screened for their improved drought, salt and/or cold tolerance according to the screening method described in Example 7 to demonstrate that transgene expression confers stress tolerance.

Example 11

Engineering Stress-Tolerant Rapeseed/Canola Plants by Over-Expressing the PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2 Genes

The constructs pBPSJyw022, pBPSJyw012, pBPSJYW030, PBPSERG010, pBPSSY012, pBPSJyw034, pBPSSY011, pBPSSY016, pBPSJyw014, pBPSJyw025, PBPSERG009, PBPSERG019 and pBPSJyw008 are used to transform rapeseed/canola as described below.

The method of plant transformation described herein is also applicable to *Brassica* and other crops. Seeds of canola are surface sterilized with 70% ethanol for 4 minutes at room temperature with continuous shaking, followed by 20% (v/v) Clorox supplemented with 0.05% (v/v) Tween for 20 minutes, at room temperature with continuous shaking. Then, the seeds are rinsed 4 times with distilled water and placed on moistened sterile filter paper in a Petri dish at room temperature for 18 hours. Then the seed coats are removed and the seeds are air dried overnight in a half-open sterile Petri dish. During this period, the seeds lose approx. 85% of its water content. The seeds are then stored at room temperature in a sealed Petri dish until further use. DNA constructs and embryo imbibition are as described in Example 10. Samples of the primary transgenic plants (T0) are analyzed by PCR to confirm the presence of T-DNA. These results are confirmed by Southern hybridization in which DNA is electrophoresed on a 1% agarose gel and transferred to a positively charged nylon membrane (Roche Diagnostics). The PCR DIG Probe Synthesis Kit (Roche Diagnostics) is used to prepare a digoxigenin-labelled probe by PCR, and used as recommended by the manufacturer.

The transgenic plants are then screened for their improved stress tolerance according to the screening method described in Example 7 to demonstrate that transgene expression confers drought tolerance.

Example 12

Engineering Stress-Tcorn Plants by Over-Expressing the PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2Genes

The constructs pBPSJyw022, pBPSJyw012, pBPSJYW030, PBPSERG010, pBPSSY012, pBPSJyw034, pBPSSY011, pBPSSY016, pBPSJyw014, pBPSJyw025, PBPSERG009, PBPSERG019 and pBPSJyw008 are used to transform corn as described below.

Transformation of maize (*Zea Mays* L.) is performed with the method described by Ishida et al. 1996. Nature Biotch 14745-50. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* that carry "super binary" vectors, and transgenic plants are recovered through organogenesis. This procedure provides a transformation efficiency of between 2.5% and 20%. The transgenic plants are then screened for their improved drought, salt and/or cold tolerance according to the screening method described in Example 7 to demonstrate that transgene expression confers stress tolerance.

Example 13

Engineering Stress-Tolerant Wheat Plants by Over-Expressing the PK-6, PK-7, PK-8, PK-9, CK-1, CK-2, CK-3, MPK-2, MPK-3, MPK-4, MPK-5, CPK-1 and CPK-2

The constructs pBPSJyw022, pBPSJyw012, pBPSJYW030, PBPSERG010, pBPSSY012, pBPSJyw034, pBPSSY011, pBPSSY016, pBPSJyw014, pBPSJyw025, PBPSERG009, PBPSERG019 and pBPSJyw008 are used to transform wheat as described below.

Transformation of wheat is performed with the method described by Ishida et at. 1996 Nature Biotch. 14745-50. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* that carry "super binary" vectors, and transgenic plants are recovered through organogenesis. This procedure provides a transformation efficiency between 2.5% and 20%. The transgenic plants are then screened for their improved stress tolerance according to the screening method described in Example 7 to demonstrate that transgene expression confers drought tolerance.

Example 14

Identification of Homologous and Heterologous Genes

Gene sequences can be used to identify homologous or heterologous genes from cDNA or genomic libraries. Homologous genes (e. g. full-length cDNA clones) can be isolated via nucleic acid hybridization using for example cDNA libraries. Depending on the abundance of the gene of interest, 100,000 tip to 1,000,000 recombinant bacteriophages are plated and transferred to nylon membranes. After denaturation with alkali, DNA is immobilized on the membrane by e. g. UV cross linking. Hybridization is carried out at high stringency conditions. In aqueous solution hybridization and washing is performed at an ionic strength of 1 M NaCl and a temperature of 68° C. Hybridization probes are generated by e. g. radioactive (^{32}P) nick transcription labeling (High Prime, Roche, Mannheim, Germany). Signals are detected by autoradiography.

Partially homologous or heterologous genes that are related but not identical can be identified in a manner analo-

gous to the above-described procedure using low stringency hybridization and washing conditions. For aqueous hybridization, the ionic strength is normally kept at 1 M NaCl while the temperature is progressively lowered from 68 to 42° C.

Isolation of gene sequences with homologies (or sequence identity/similarity) only in a distinct domain of (for example 10-20 amino acids) can be carried out by using synthetic radio labeled oligonucleotide probes. Radio labeled oligonucleotides are prepared by phosphorylation of the 5-prime end of two complementary oligonucleotides with T4 polynucleotide kinase. The complementary oligonucleotides are annealed and ligated to form concatemers. The double stranded concatemers are than radiolabeled by, for example, nick transcription. Hybridization is normally performed at low stringency conditions using high oligonucleotide concentrations. Oligonucleotide Hybridization Solution:

6×SSC
0.01 M sodium phosphate
1 mM EDTA (pH 8)
0.5% SDS
100 μg/ml denatured salmon sperm DNA
0.1% nonfat dried milk

During hybridization, temperature is lowered stepwise to 5-10° C. below the estimated oligonucleotide Tm or down to room temperature followed by washing steps and autoradiography. Washing is performed with low stringency such as 3 washing steps using 4×SSC. Further details are described by Sambrook, J. et al. (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F. M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.

Example 15

Identification of Homologous Genes by Screening Expression Libraries with Antibodies

cDNA clones can be used to produce recombinant protein for example in *E. coli* (e.g. Qiagen QIAexpress pQE system). Recombinant proteins are then normally affinity purified via Ni—NTA affinity chromatography (Qiagen). Recombinant proteins are then used to produce specific antibodies for example by using standard techniques for rabbit immunization. Antibodies are affinity purified using a Ni—NTA column saturated with the recombinant antigen as described by Gu et al., 1994 BioTechniques 17:257-262. The antibody can than be used to screen expression cDNA libraries to identify homologous or heterologous genes via an immunological screening (Sambrook, J. et al. (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F. M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons).

Example 16

In Vivo Mutagenesis

In vivo mutagenesis of microorganisms can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W. D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those skilled in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34. Transfer of mutated DNA molecules into plants is preferably done after selection and testing in microorganisms. Transgenic plants are generated according to various examples within the exemplification of this document.

Example 17

In Vitro Analysis of the Function of *Physcomitrella* Genes in Transgenic Organisms

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one skilled in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E. C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N. C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P. D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswangcr, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H. U., Bergmeyer, J., Graβ1, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, Enzymes. VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. et al. (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as β-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R. B. Pores, Channels and Transporters, in Biomembranes, Molecular Structure and Function, pp. 85-137, 199-234 and 270-322, Springer: Heidelberg (1989).

Example 18

Purification of the Desired Product from Transformed Organisms

Recovery of the desired product from plant material (i.e., *Physcomitrella patents* or *Arabidopsis thaliana*), fungi, algae, ciliates, *C. glutamicum* cells, or other bacterial cells transformed with the nucleic acid sequences described herein, or the supernatant of the above-described cultures can be performed by various methods well known in the art. If the desired product is not secreted from the cells, can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonification. Organs of plants can be separated mechanically from other tissue or organs. Following homogenization cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from desired cells, then the cells are removed from

the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One skilled in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There is a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J. E. & Ollis, D. F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986). Additionally, the identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek et al., 1994 *Appl. Environ. Microbial.* 60:133-140; Malakhova et al., 1996 *Biotekhnologiya* 11:27-32; and Schmidt et al., 1998 *Bioprocess Engineer.* 19:67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. et al. (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

APPENDIX

Nucleotide sequence of the partial PK-6 from *Physcomitrella patens*

(SEQ ID NO: 1)

```
GCACGAGCTCAATCCTCATGTTTCGGACTGTGGACTAGCTGCCCTTGCACCATCTGG
TTCTGAACGCCAGGTGTCGGCACAAATGTTGGGCTCTTTCGGTTACAGTGCCCCTGA
GTACGCCATGTCTGGAACCTATACCGTGAAGAGTGACGTCTACAGCTTCGGTGTTGT
AATGCTGGAGCTACTCACTGGGCGCAAGCCTTTAGACAGCTCAAGACCACGATCCG
AGCAATCTTTGGTACGATGGGCCACACCTCAATTGCACGACATCGACGCCCTTGCAC
GAATGGTGGATCCGTCGTTGAAGGGCATCTACCCTGCTAAATCACTCTCTCGGTTTG
CTGATATAGTCGCCCTTTGCGTCCAGCCGGAGCCCGAGTTCCGACCCCCGATGTCTG
AAGTGGTGCAGGCACTTGTAAGGCTGATGCAGCGTGCGAGTCTGAGCAAACGCAGA
TCGGAGTCCGCTGTTGGGAATTGAGTCGAACGAGCCATCTGAGACTTCACCTTTGAG
AGTACTGAAGCGCCCACTAGCCTAATCGTGCATCTTTGGCCATCTCGTTTCTGAGTG
GAACACAAAGCTGGGTATATTCTTTGGTGGTTAAGCAACCATTTGTCCCAATTTGAA
CTTCCGCTGGNGAAGGTCTGTATGTTGAGAAACGATGCAAAGCGTTCGCGTGGTNTG
CTTGAACTTCAAA
```

Nucleotide sequence of the partial PK-7 from *Physcomitrella patens*

(SEQ ID NO: 2)

```
GCACGAGCTCAATCCTCATGTTTCGGACTGTGGACTAGCTGCCCTTGCACCATCTGG
TTCTGAACGCCAGGTGTCGGCACAAATGTTGGGCTCTTTCGGTTACAGTGCCCCTGA
GTACGCCATGTCTGGAACCTATACCGTGAAGAGTGACGTCTACAGCTTCGGTGTTGT
AATGCTGGAGCTACTCACTGGGCGCAAGCCTTTAGACAGCTCAAGACCACGATCCG
AGCAATCTTTGGTACGATGGGCCACACCTCAATTGCACGACATCGACGCCCTTGCAC
GAATGGTGGATCCGTCGTTGAAGGGCATCTACCCTGCTAAATCACTCTCTCGGTTTG
CTGATATAGTCGCCCTTTGCGTCCAGCCGGAGCCCGAGTTCCGACCCCCGATGTCTG
AAGTGGTGCAGGCACTTGTAAGGCTGATGCAGCGTGCGAGTCTGAGCAAACGCAGA
TCGGAGTCCGCTGTTGGGAATTGAGTCGAACGAGCCATCTGAGACTTCACCTTTGAG
AGTACTGAAGCGCCCACTAGCCTAATCGTGCATCTTTGGCCATCTCGTTTCTGAGTG
GAACACAAAGCTGGGTATATTCTTTGGTGGTTAAGCAACCATTTGTCCCAATTTGAA
CTTCCGCTGGNGAAGGTCTGTATGTTGAGAAACGATGCAAAGCGTTCGCGTGGTNTG
CTTGAACTTCAAA
```

Nucleotide sequence of the partial PK-8 from *Physcomitrella patens*

(SEQ ID NO: 3)

```
GCACCAGACTATGACAAGCGCACGCCCTTGCACATCGCCGCGTCCCTGGATTGTGTC
CCTGTTGCTAAAGTCCTGCTTGCGGAAGGAGCAGAGTTGAATGCAAAAGACAGGTG
GGGGAAATCTCCGAGAGGCGAGGCGGAGAGTGCAGGATACATGGAGATGGTAAAG
CTGTTGAAGGATTACGGGGCTGAGTCACACGCAGGTGCCCCGAGGGGCCACGTTGA
GAGTCTGATTCAGGTTGCCCCTCCGTTGCCTTCTAACCGCGACTGGGAGATCGCTCC
GTCGGAGATTGAACTTGATACCAGCGAGCTCATCGGCAAAGGCTCCTTTGGAGAGA
TTCGGAAGGCGCTTTGGCGCGGCACACCCGTCGCTGTGAAGACAATCAGACCTTCTC
TGTCCAACGACAGAATGGTCATCAAGGACTTCCAGCACGAGGTGCAATTGCTCGTA
AAGGTTCGGCACCCAAACATTGTGCAGTTCCTCGGGGCTGTTACCCGTCAAAGACCT
CTCATGTTAGTCACCGAGTTTCTGGCAGGGGGGCGATTTGCATCAGTTGCTGAGGAG
CACCCTAAATTTGGCTCCTGACCGCATCGTGAAGTATGCCCTCNACATAGCTCGCGG
CATGTCTTACTTCACCATCGGAGCAGCCCA
```

Nucleotide sequence of the partial PK-9 from *Physcomitrella patens*

(SEQ ID NO: 4)

```
TCCAGCCCATTTGGTTGGCCACACACAGCTGTTCATGAGTCACCCGCTTCAGGNTGA
ACTGAAGAAACGTAACTCCGTACGGCTATTTTACCAAATTTTCAAGCTCGTTGTCCC
GCCATGATCCAAATGGAAGCTCAGTTTGCAACATGAAGTACATTGAACACACCTACC
GCCCACCAGTCAGAAGCCAGGCCATGACCTTGTCCTTGAATGATCTCGGGTGCTAAG
```

AAATCAGCCATGCCACAGACTGTGAAAGTGCGCTCATCCGACATTTGCTTTGCAAAC
CGAAAATCAACCAGCTGAAGTCGTCCTTTCCGATCTATCATAAGAACATCGGGAGA
GATGCCACGATATACAACGCCATCCTTGTGCAGAAGTTCGACGGCTAATACCACGTT
GGCGACCAGAAAACGAGCTGAGTTCTCGTCTAAAGGTGACCGAAGTAGAAGTTCTA
GAGGCCCAGCTAACACACAATTAAGAACGAGTGCCACATTGTCACTGTCAATAGGG
GTGGCCAAGAGATGCGGCACGAATGGGGAAGGCCTCAGTTGCTTGAAAAGAGTTCT
CTCCAATAGGACTTGGCCCTCCCGACCGAGTCTCTGAACTTTACGTCTCTGGTACCTT
TTCATGCTTATGACGTCATCTGATTTCTTGCAGAGCACCACACCGACATCACAGCAA
TCGGTTGAATAGACCTGGTGCCGATTCCT

Nucleotide sequence of the partial CK-1 from *Physcomitrella patens*

(SEQ ID NO: 5)

TATGCCCATCTTCTCATACTCAGACCAGATCCTCTATTTCAATTACAGAAGAAAGTT
GCTTGTGCAACGTATTGAAATCATCACCGTCATGGGCTTTCCGAGTAAAAATTCTTG
TAATGGATAAAGTCATTTCTAGTCTGATCCATACAAGCTACCGACACAATGCTAGAA
GCCTTGATTTACACACTACACACTAGAGAGTCTACAACTCTTTTCCTACACTCTGCTT
AGTTGCCTCATCCTCAACTCCATAAACCCCCATTCACAATCATGTAAGACTTGAGAG
AGGGAAACAGTAAGCAACCTTGTGCTATTTTAGTACCAGAGCAGAGGATGAACCAC
TAGTCCTCCCAACGTAAGCCCTAATTCGCCGCAACAACCTCACGACGGAACTCCGAC
TTGGTCAAGGGTGGACAATATGATACATTCGAAGGTCGATTTTGCAAATGGGACGA
AGCAGCGGAATTCTGGCTGCGCACTGATTGCAGAGAGCCATTCTGGGGGAGTTGAG
TATACACAGTCCAGTCGTACACATGGTCGAGCTGGAATTTTTTCTGAATGAAAAGAT
CACGGAACAAGCTTCGGAGGTACAGTAGTCAGGCTGCTCGTAAAAACCTANACTTC
GCGGCGTGGTGCAAAAAGTCGGCAAATTGACTGGGATACCCATCACAAAGCTCCTC
CCACAGTGGGGGTCATCTTGATTTTGTTGTGCATGTACTCGTGTTGCTTCTGGTCAGT
GAGGGCGTTGCCCGCCCTTCCCTTGCCATGGCAAATTGCCTCTTAGAAAGTACATAA
GAATGTAACCCAAGTGATTCTATGTCATCTCTTCTACTGTGCTCGATTCCTCTGTGCT
GATTCCTACTAGCGTACCGTGCCGTCCCTGTGAAGCTCTTCCTATCTCGGTAAGGGA
TATGCCTTCGTGTTGCCGGGTCCATGTACTCCTTTGCCAAGCCAAAATCTATAATGA
ACACTTGGTTTCCTTGCCGACCGCAGCCCATGAGGAAGTTATCCGGCTTCAGGTCAC
GGTGAACGAGCCCTCGAGAATGCACGTATTCCACCCGGTCAATCATTTGGTAACCGA
GCATAATCACGGTCTTCAACGAAAACCTTAGCCCACACACCTTAAAGAGGTGCAAC
AGGTTCGGCCCCAATAGGTCTAGCACCATCACATTGTAGTCTTCTGCTGCTTTTCCGA
ACCATCTCATGTTGGGCACTCCCTTCCCACCCCGCAATATGTTGTACAAGCGCGACT
CGTGCATTAACTCTCGTGC

Nucleotide sequence of the partial CK-2 from *Physcomitrella patens*

(SEQ ID NO: 6)

TTTTTTTTTTCCAATAGATTTGCATTACATAACTCCAAGTTATGATATGTACAGGTTA
GCAACAAGCTAATGGCTGCAAGCAGTGAACATACTACCAAGGGAGAGATTCTCACT
CCCTAGACTTCATCCTCGTACGTTACTTGGCAAGGATTATGGTTTAGTGATAAAAAG
CTTCACAAGCCGGCAAGCATGCTGGTTGCTTCTGCTGCAATCTAATGATTATTTCCTT
AGGAATCGTATGGCAGAGAGCTACCACACAAAGCACTGACAATGGTTTGATGGTAA
CAAGATAGAGATCCATTCATTCCTAAGTATGAGAGACCTGTAGTCTTAGCACCATTG
TAGGACAGAACCACCGTTTTCCCCTCAATCAGGCTGTTGCCAAATGTAGAGCAACTC
TCATCAACATAACAAGAGGGTTTGATAGAAGACAGAGCCCGGCTATATAACCACAA
GCCCTGCGCCTACCTTATAACGGCTTGGATCCACCTCAACAGAAAGTGATTCAACTC
CCTTGATACCGGCTTTCGTAAATCCTCAAGTTGGCAGATGGCGGTTGTGGATGGCGG
CTAGATATCCGCTTTGGGTCCGAAGTAACTGGAGAGCTCCTCTGCATCCCTGCTGAC
GACCGTAAGCTGGTGGGACCAAGCTTACTGCTCCCTGTTCGAGAGGAATCTACGACT
TCTGCTGATGCCCCTGAGGGCCTGCTGCTAGATAGGACAGCTCGCCTGGAGGAAGA
ACCCCCCCGAGTTGCATACGAAGATGTATGCATGCGCTCTGGTTCTGACACAACAGC
AAGAGCAGAATCCTTAGCAGATTCATCAAGTCCAGGACTTTTGTGCTTAGATGAGTC
CAAAGCATTTGCGACCCCGGAGCCATTTGCTCCTCCAGGAAGCCTGCGCCGAGAAG
GATCCATTGGTTCGGTGGGCCGCTGCAGGTCTCGGCTTCCTGTAGCCCCAGTTCCAA
GTGCACCACTGGTTTGCCCTGCAGAAGCACCCAGTCGAGTTGAACTGCCACCGGAA
ATTTGTGACTGCTGGTACTTCAGAATTGTCCAGTCAAAAACGTAGTCAAATTGAAAA
CCTGTAAAACTATTTCCAGTTTAGGCAAACAGAAGTGGCACTGTAATAAACTGAAAA
TCATCAAACATTCACAAACTATCTGTTCGTTGATAGAGCATAGTAAAGTCTGCGCTT
AGGATCAAGTCTTGATACATTACAATGCCCAAGCAAGAGTGAAACCTACAAAAGTT
ACAGTTTTCATACCCTCACGAATAAAGAGGTCACGGAAGATTCTTTTCAAATATGCA
TAGTCGGGTTTGTCATCAAAACGCAAGGACCGGCAGTAGTGGAAGTACGCTCGTGC
GAATTCTGAAGGATAATTTTTACAAAGGACCTCAATGGGCGTGGACATTTGTTTTCT
CACTGATCTTCTCGTACTTCTGCTTCTTGGTTCCCGCTTTCAGTCCTTGCCCATGGAA
GACTGCCTCTCAGGAAGTACATGAGCACATATCCAAGAGATTCCAAATCATCTCGTC
TGCTTTGCTCAATACCAAGATGAGTGTTGATGCTTGCATACCGAGCAGTCCCTGTCA
GATTTTTGTTCTCCCTGTAGGGAATATGCTGATGCGTGGAAGGGTCGCGGTACTTCTT
GGCAAGACCAAAATCAATAATGTAGACCTGGTTTGCTCGCCTACCAAGCCCCATTAG
AAAATTATCAGGCTTGATGTCTCTATGAAGAAAGCTTTTCGCATGCACATACTCCAC
TCTGTTGATCAGCTGGTCAGCAAGCATGAGAACAGTCTTTAAAGAGAACTTCCGGCT
GCAGAAGTTGAAAAGGTCTTCGAGACTTGGCCCCAACAGATCCAGAACCAAGACAT
TGTAGTCTCCTTCTATCCCGAACCATCCTCGTGC

APPENDIX-continued

Nucleotide sequence of the partial CK-3 from *Physcomitrella patens*

(SEQ ID NO: 7)

CGGTGGGGCGCTCCCCAATATTTTATCCCCGGGGCTGCAGGGAATCCGGCGACCAGT
NTTTGAAGGTGTCAACGCCGTGAATAGTGAGCGTTGCGTTATGAAGATTTTGAAGCC
AGTAAAGAAAAAAAAAGATCAAAAGAGAGATCAAGATTCTGCAAAACCTTTGTGGAG
GGCCCAACATTGTGAAGCTTCTGGACATTGTCCGTGATCAGCAATCGAAGACACCCA
GCCTAATTTTTGAGTATGTGAACAATACTGATTTCAAAGTGCTCTACCCCACTCTTAC
AGACTTTGATATCCGATACTACATTCATGAGCTGCTCAAGGCTTTGGACTATTGCCA
TTCTCAAGGGATTATGCACAGGGATGTGAAGCCACACAACGTGATGATTGACCATG
AGCAGCGGAAGCTTAGGCTTATTGACTGGGGACTTGCCGAATTCTATCATCCTGGCA
AAGAGTATAATGTGCGTGTTGCCTCTAGGTACTTCAAGGGTCCTGAGCTGCTGGTTG
ATCTTCAAGATTATGATTACTCTCTCGACATGTGGAGCTCTGGGGTGCATGTTTGCCG
GCATGATATTTCGGAAGGAGCCATTCTTTTATGGGCATGACANTTCATGATCAACTT
GGTGAAGATCGCTAAGGTGTTGGGAACTTGATGAATTGAATTCCTATCTAACAAATA
CCGCTAAGTGGACCCCATTGGAGCACCTGGTGGGGG

Nucleotide sequence of the partial MPK-2 from *Physcomitrella patens*

(SEQ ID NO: 8)

GCACGAGGAACTAACGAATTGTCATTCTATAATCCAATAGTGTAATCACACGGGGG
GGAATAAGTTGCAAAACCATACAACGCCGGGATAGCGTTGTAGCCACCTAAAGAAT
TGAGAGTAGGCCTTACAACTTGAGATGAAGTGTGAAGTGGTACTGCACCATATCATC
AGGACCTAAGCTGCAATCCAGAGCCTCCCTCCAAATGAGATCCCTGATAGGCTCCTC
CGAGATAGAGGGCTCCTCGAAGCCAAACTCGAAGGGAGATACCGAGCCAGGCTCAT
CGTTGATGTCATGAAGTGAAGCTTAAATAAGGGTGCGCCAAGGCAGCTTCCACTGTG
ATTCTTTTCGCTGGATCAAAGACCAGCATCTTTTCAACAAGATCAAGAGCAGAACGA
TTAATGCCTCTGAACTTCTGGGTTAAGGGAATAGGCGACTGTCGAGGCAGGTGCTTG
ATATACCGCCTAGCATTGTCGCTTCTCAAAAACCCAAGATCCCTATCTTCAGGAGTT
CCGATGAGTTCTGTAATTAGGCGGAGCTGATGCACATAGTCTCTCCCAGGGAACAAC
GCAGATCGGTTAAGCAACTCCATGAAGATGCACCCCACAGACCAAATGTCAATAGC
TGCAGTGTATGCTGAACAATTCAGGAGCAGCTCTGGAGCTCTGTACCACCTCGTTAC
AACATACTCAGTCATGAAATCCGTTTCAGAGAGAGTGCGTGCCAAGCCAAAATCTG
CGATTTTCAAATCGCAATTGGCATTGACGAGAAGGTTGGTGGGCTTCAAGTCCCGGT
GCAAGACGTTCGCCGAATGGATGTACTTCAAGCCCCGCAAGATTTGATACAGAAAA
TACTGACAGTGGTCTTCTGTGAGAGCTTGATTTGAACGAATGATCTGGTGTAGGTCC
GTATCCATCAACTCGTATACAATGTACACGTCGTTGAAATCTCGTGC

Nucleotide sequence of the partial MPK-3 from *Physcomitrella patens*

(SEQ ID NO: 9)

CGGCACCAGCCTCGCTGGAGACCGACCATCGAAGCACCTTAAGCTCGTTTTCATTCG
GCATTGCTTGCGAGCACTTCGACTTCCTAGAATTTCAATAGACCTAATGGAATCGCC
ACTCCCTAATCTTTCCGGAGAGGCCTTATCGCCGACGGCAACTGCCGAAGACGAGAT
TACTCAGATGATACTAAAAAGTGCCGCAAGGTCCGAATTAGGAATGTATGTTTCGAA
GAGACAGGAATTCTATCTTCGAAGAGCGCGGAGGCGGCGTAAGTTTGCGTGGAAGC
CGGTTTTGCAGAGCATCTCCGAGATGAAGCCTGTCATGGAATTCCACACTCCGATGG
CTTACCGGGATAGTGGGTCTCCGCCGAAGAACGCCTCTACCCCATCCTTACCTGGCC
CGAAGAACATTTCACCGCCACGACAAGTGAGTGTCCCGCAAAGGAGCAGTCCTCCG
CCGAAGAACGTCTCACCACCTCCCCAGCCCGGCATTTTGTAGCGCGGACTGCGATCG
AAGTATTCTGCTGCATCTCAGCAAGTTCAACGAAATCGAGGGCAACGCGAAATCTCT
TTTATATGGCGTAGTTTGTGTCTCCGACTGGACTCCTATCTATCCCCATCGAGATAAC
TGATTCGGTGGATAATTTCTCCAAATTTTGGCTAACNCAAGAANCTCAAGGGCGAAT

Nucleotide sequence of the partial MPK-4 from *Physcomitrella patens*

(SEQ ID NO: 10)

GCACGAGGTTGGTGTAAGTTATTGATAGTGCTGTGCAATTCACAGTTTTGCTACTCC
GGTAGGTCCGACCTCTTCAATTGTCAGTTTAAAAACTCTAAAAACATTTGAGAAAAG
TGTTGAAAAATCTCCGTGAGGAAATTCCTTGTCGCAAGACGTGAAAAAAAGAAGAA
AGAAGATGGAAATATTGTTTTGGGTATCGAAGAAGTGTTCGATGCTGTGCAATAAGG
AAAGAAAAAGTGCAGGTAACATAAAAAGCTAGCATGGTGATGATAATATAAGACCC
CGATTAACACACTTATGGATTGTTTCATGAGCTGCACGTTCTCAGCGACAAATGGGG
CTCATTGAGAAAACTCCACTTTCTATAAGGTTGGGAAACGAGCGTTTTTTTTTTGAAG
ATGTTTTTTCCGTCAATCTGATTTGATATCGTTCTCAACTTGACCACATATGACTATA
TAAGGAAAAGGCATTGAGAAAGTGGCGGATTGGCGAGGTAGTTCGACCATGCTTTT
GGTAAAGTCCCTTGAAGTTCAGTGGTGGATCAGGCTTGTGGTAGTGACAGTCTCTGC
ACGCCATGCGAGGCTAACTTTAAGTTACAAAATCTTGCTCAAATGGTACTCTTCCTC
GTTGTACTTTTGCAGGAACGGATGTTTAAGTAAATCAGTAGTTGATGGTCGTTCACT
GGGACATTTCCGGATGCAGGATTCAATAAAAGAACAAAATTCGGGGGAGAATTTGT
CAGGGGATGCGGCTGCGGGGGGTTGATTAACTATACATTCCATGAGGATGAAGAAA
TTTTGCCAACCCTCTTCCATTCCAGCTGGTTTGTATGGGAAGGTACCCAACGCACACT
CCAAAAGAGTCAATCCTAAACTCCATAGGTCACTGTCGTATGCATACGAACGCCCCT
GAAGGCGTTCTGNCGACATATATGTGCAAGTCCCAACGAACGTGTCTCGCTGGGCCA
AGGAATGAACCAACACAGCACTGACACCAAAATCAGATATTTTGACCTCACCCTTGT
GATTGATGAGGAGGTTGGAGGGCTTTATATCACGATGTATGATGTGCCTGACTTGGT
GTAGGTATTCCAATCCCTTCAGAACTTGACTAGCAATGACGGCCAAATACGGCTCAG
GTATNTGCTTTCTGGTGC

APPENDIX-continued

Nucleotide sequence of the partial MPK-5 from *Physcomitrella patens*

(SEQ ID NO: 11)

TCCCCGGGCTGAGGAATTCGGCACGAGCGGTTGATCCTCACCCTTGGGAAGGACCCT
GGAATTGAGTAGCGTGCGGAAGCTGCATCGATCCGGAAGAGACGATGAGTAGGAGA
GTGAGAAGGGGAGGTCTTCGCGTCGCGGTGCCGAAGCAAGAGACTCCCGTCAGCAA
ATTTTTGACTGCCAGTGGAACTTTCCAGGATGATGATATCAAGCTCAACCACACCGG
GCTTCGCGTCGTCTCTTCAGAACCTAACCTTCCTACGCAGACGCAGTCTAGCTCCCC
AGATGGGCAACTGTCAATAGCAGACCTGGAGTTAGTGCGGTTCTTAGGAAAGGGTG
CGGGTGGAACCGGTGCAGCTTGGTCCGGCACAAATGGACCAATGTCAATTATGCAC
TGAAGGCGATACAAATGAATATCAACGAAACAGTGAGGAAGCAGATTGTTCAGGAG
CTGAAAATCAACCAAGTGACGCACCAGCAGTGCCCTTATATCGTGGAATGCTTCCAC
TCCTTCTACCACAACGGCGTCATATCCATGATCCTAGAGTACATGGACAGGGGCTCG
TTGTCCGACATTATTAAGCAACAAAAGCAGATACCTGAGCCGTATTTGGCCGTCATT
GCTAGTC

Nucleotide sequence of the partial CPK-1 from *Physcomitrella patens*

(SEQ ID NO: 12)

GCACCAGCCGAGTCGGGCATTTTTCGTGCGGTGTTGAGGGCTGACCCGAGCTTTGAA
GAAGCCCCTTGGCCTTCCATCTCTCCCGAAGCCAAGGATTTCGTGAAGCGTCTCCTG
AATAAGGATATGCGGAAACGCATGACTGCTGCACAAGCTTTAACTCATCCATGGATT
CGAAGTAACAACGTGAAGATACCTCTGGATATCTTAGTGTACAGACTTGTGAGGAAT
TATCTTCGTGCATCATCCATGAGAAAGGCTGCTTTGAAGGCCCTGTCAAAGACTTTA
ACCGAAGACGAGACTTTTTATCTACGTACTCAATTTATGCTGCTAGAACCAAGTAAC
AACGGTCGTGTTACTTTTGAGAATTTCAGACAGGCACTGCTGAAAAATTCAACAGAG
GCCATGAAAGAGTCACGGGTTTTTGAAATTCTGGAATCGATGGATGGTCTTCATTTC
GCACCAGCCGAGTCGGGCATTTTTCGTGCGGTGTTGAGGGCTGACCCGAGCTTTGAA
GAAGCCCCTTGGCCTTCCATCTCTCCCGAAGCCAAGGATTTCGTGAAGCGTCTCCTG
AATAAGGATATGCGGAAACGCATGACTGCTGCACAAGCTTTAACTCATCCATGGATT
CGAAGTAACAACGTGAAGATACCTCTGGATATCTTAGTGTACAGACTTGTGAGGAAT
TATCTTCGTGCATCATCCATGAGAAAGGCTGCTTTGAAGGCCCTGTCAAAGACTTTA
ACCGAAGACGAGACTTTTTATCTACGTACTCAATTTATGCTGCTAGAACCAAGTAAC
AACGGTCGTGTTACTTTTGAGAATTTCAGACAGGCACTGCTGAAAAATTCAACAGAG
GCCATGAAAGAGTCACGGGTTTTTGAAATTCTGGAATCGATGGATGGTCTTCATTTC
AAGAAAATGGACTTTTCAGAGTTCTGTGCAGCGGCCATTAGTGTTCTCCAGTTAGAA
G

Nucleotide sequence of the partial CPK-2 front *Physcomitrella patens*

(SEQ ID NO: 13)

GCACGAGCTCCTGCATCTCCCCCTCCTTCTCCTCCTCATCATTCTGGAGCCCAGCGAA
CTGCGATCTGAGATTCCAACTTGGAAGGGCCTCGCGTAAGCACCGGAGCTCGTTTCT
TACGCTTTTGCGCCTCGCGATATTTGTACATTGTTTCCTCTGGTTTTATTCGATTCCGC
CTCTGAAAATGTGAACGGGCTGCAAGCTTGGTTTTGGAGCAACGTTGGAGCATTGAA
GGGTTGCGCTCGTCCCTGCCCATTCCTCGCTTCTGCTCTGGCCTATGTCATGACGACG
TGAAGGAGAGGATTTGAGGGTTTTGCAAGTGATATAATCCTCCCCGAGGAGATTTCT
GTGAGTTGATTAACTTGGATCAGCGACATGGGGAACACTAGTTCGAGGGGATCGAG
GAAGTCCACTCGGCAGGTGAATCAGGGAGTCGGGTCTCAAGACACCCGAGAGAAGA
ATGATAGCGTCAATCCAAAGACGAGACAGGGTGGTAGCGTTGGCGCAAACAACTAT
GGCGGAAAGCACAAGCAGTGGTGCTCAGGCCGGAGAACGATCCACCTCTGCGCCCG
CTGCTCTGCCGAGGCCGAAGCCAGCATCGAGGTCAGTATCCGGTGTTTTGGGTAAGC
CGCTGTCAGATATTCGTCAATCTTACATCCTGGGACGGGAGCTTGGCCGAGGGCAGT
TCGGAGTGACTTACTTGTGTACTGACAAGATGACGAATGAGGCGTACGCGTGCAAG
AGCATCGCCAAACGGAAACTGACCAGTAAGGAGGATATCGAGGATGTTAAGCGGGA
GGTTCAGATTATGCATCACCTGTCGGGGACACCCAATATCGTGGTGTTAAAGGATGT
GTTCGAGGACAAGCATTCCGTGCATCTTGTGATGGAGCTCTGTGCAGGTGGCGAGCT
CTTCGATCGCATCATTGCCAAGGGGCATTACAGTGAGCGCGCCGCTGCCGATATGTG
CAGAGTCATCGTCAATGTGGTGCACAGATGCCACTCATTAGGGGTCTTCCATCGGGA
TCTCAAGCCAGAGAATTTTCTGTTGGCCAGCAAGGCTGAGGATGCGCCTCTGAAGGC
CACAGACTTCGGTCTGTCAACTTTCTTTAAGCCAGGAGATGTGTTCCAGGATATTGTT
GGAAGTGCGTATTACGTGGCCCCTGAAGTTTTGAAGAGAAGTTATGGTCCTGAGCTG
ATGTTTGGAGTGCAGGCGTGATTGTGTACATTCTGCTGTGTGGTGTACCCCCCTTCTG
GGCTGAAACTGA
GCAGGGTATCTTTGACGCTGTGCTCAAAGGGCACATAGACTTCGAGAACGAGTCCAT
GGCCGAAAATCTCCAACGGGGCTAAGGATTTGGTGAGGAAAATGCTAAACCCTAAC
GTGAANAT

Nucleotide sequence of the full-length PK-6 from *Physcomitrella patens*

(SEQ ID NO: 14)

ATCCCGGGTGAGTATCACTTACGGTGGCGAGGGATGGCCTTTGGGGTAGGAGCTGGT
ATATGCGGAGTCCAACAGAAGCTTGTGCAGGACTCTTGAGTTGTGCGTGCGAGGGCT
GAGTGCCGGAAAGGTATTTTCCGACGAAGAGTCAATGTGGGCGTGGACAAACGTTT
GAAGAGATGGGTGTGGATATGAAGGCTCCGGCTAAGCAGTCGCTGGGAGTCGGACT
GCTCCTGTGCTCTGTAGTGATCCTCTCGGTGGTGAGCTCTGTGTATGGCCAAGTTCAG
ACAGATCCAGTGGATACTACAGGCTTAATTTCCATGTGGTATGACTTAAAACAGAGT
CAATCTCTCACGGGGTGGACTCAAAATGCTTCTAACCCTTGTGGGCAGCAGTGGTAC
GGCGTTGTATGTGATGGCTCTTCTGTCACGGAAATCAAAATTGGAAGTCGGGGTTTG
AATGGAAATTTTAATCCTTCGTACTTTCAAAACGCTTTTAAAAAGCTTCGAATTTTTG

APPENDIX-continued

ATGCTAGTAACAACAACATCGAAGGAAATATTCCTCAACAGTTTCCTACGTCTCTTA
CTCAAATGATATTGAACAACAATAAATTGACCGGAGGTCTCCCACAGTTTGATCAAT
TGGGCGCCTTGACAGTCGTAAACTTGAGCAACAACAATCTGACCGGCAACATGAAC
CCCAACTATTTCAATGTGATCGTGAATGTGGAAACCTTCGATGTTTCCTATAACCAA
CTTGAAGGCACTCTTCCCGACTCCATTCTAAACCTGGCCAAGCTTCGTTTCTTGAATT
TGCAGAACAATAAATTTAATGGTAAACTTCCCGACGATTTCTCTCGGCTGAAGAATT
TGCAGACTTTCAACATTGAGAACGATCAGTTCACGGGTAATTATCCATCAGGTTTAC
CCAGTAATAGCAGGGTTGGAGGAAATCGTCTTACATTTCCCCCACCTCCAGCCCCCG
GCACACCTGCTCCCAGGACTCCTTCTCCTTCAGGAACATCGAATGGATCATCGTCGC
ATCTCCCTCTAGGGGCGATCATTGGAATAGCCGCTGGTGGTGCTGTGCTGCTTTTATT
ACTAGCACTCGGCATCTGTTTGTGTTGTCGTAAGCGGTCCAAGAAAGCATTGGGCGA
TCCAGAGGCCACGACCAGCAGCCGAAGACCGTGGTTCACACCTCCCCTCTCCGCAA
AGAGCCAGAGTGATCCCAGCAAGAGCATAGACAAAACGACGAAACGCAACATCTTT
GGCAGCAGTAAGAGTGAGAAGAAAAGTTCAAAGCACAGAGTATTTGAGCCAGCTCC
TCTTGACAAAGGAGCAGCCGACGAACCAGTGGTGAAGGCGICTCCGCCCGTCAAGG
TACTGAAGGCTCCTCCTTCATTTAAGGGTATCAGCGGCCTGGGTGCTGGACATTCGA
AAGCAACAATTGGCAAGGTGAACAAGAGCAATATTGCAGCCACCCCATTCTCTGTA
GCGGATCTTCAGGCAGCCACAAACAGCTTCTCCCAGGATAATCTGATTGGAGAAGG
GAGCATGGGTCGCGTGTATCGTGCCGAGTTTCCCAACGGCCAGGTCTTGGCCGTGAA
GAAGATCGACAGCAGCGCGTCGATGGTGCAGAATGAGGATGACTTCTTGAGTGTAG
TAGACAGTTTGGCTCGCCTGCAGCATGCTAATACGGCTGAGCTTGTGGGTTACTGTA
TTGAACATGACCAACGGCTGTTGGTGTACGAGTACGTGAGTCGTGGAACCCTGAAC
GAATTGCTCCATTTCTCGGGTGAAAACACCAAGGCCCTGTCCTGGAATGTCCGCATT
AAGATTGCTTTGGGATCCGCGCGTGCTCTGGAGTACTTGCACGAAGTCTGTGCACCT
CCCGTGGTTCACCACAACTTCAAATCTGCCAATATTCTGCTAGACGATGAGCTCAAT
CCTCATGTTTCGGACTGTGGACTAGCTGCCCTTGCACCATCTGGTTCTGAACGCCAG
GTGTCGGCACAAATGTTGGGCTCTTTCGGITACAGTGCCCCTGAGTACGCCATGTCT
GGAACCTATACCGTGAAGAGTGACGTCTACAGCTTCGGTGTTGTAATGCTGGAGCTA
CTCACTGGGCGCAAGTCTTTAGACAGCTCAAGACCACGATCCGAGCAATCTTTGGTA
CGATGGGCCACACCTCAATTGCACGACATCGACGCCCTTGCACGAATGGTGGATCCG
TCGTTGAAGGGCATCTACCCTGCTAAATCACTCTCTCGGTTTGCTGATATAGTCGCCC
TTTGCGTCCAGCCGGAGCCCGAGTTCCGACCCCCGATGTCTGAAGTGGTGCAGGCAC
TTGTAAGGCTGATGCAGCGTGCGAGTCTGAGCAAACGCAGATCGGAGTCCGCTGTT
GGAATTGAGTCGAACGAGCCATCTGAGACTTCACTTTGAGAGTACTGAAGCGCCCA
CTAGCCTAATCGTGCATCTTTGGCCATCTCGTTTCTGAGTGGAACACAAGCTGGGTA
TATTCTTTGGTGGTTAAGCAACATTTTGTCACAATTTGAACTTCAGCTGGAGAAGGG
TCTGTAGTGTTGAAGAAAACGAATGCAAAGCGTTTCGGCGTGGATGTGCTTTGAGAA
CTTACAAAACTCATCAAGACTTTGAAGATCTTTGTATTGCATCGAATCCTTTCAATCA
GTCTCGGGTAGGATCAGTTCCTCTGTATCGGATACCCTTTTCATCCTAACATGGGACC
CTTTTAATCCAGAGGATGGAGTGCTTGGAATAGTGACCTTGGTCGAGTTAACGC

Nucleotide sequence of the full-length PK-7 from *Physcomitrella patens*

(SEQ ID NO: 15)

ATCCCGGGAGTGGGTGGTTGGACTGTAAGGAGCTAGCGTTTTAGAGCTACAGTGCG
GTTTGCTGTGTGAGTGAGTGAGTGAGTGCGTGAGTGAGGATGTCTGTTTCTGG
TATGGACAACTATGAGAAGCTGGAGAAGGTAGGAGAGGGGACTTACGGAAAGGTGT
ATAAGGCCCGTGATAAACGCTCCGGGCAGCTGGTGGCGCTCAAGAAGACTAGGTTG
GAGATGGAGGAAGAAGGCGTCCCTTCCACCGCTTTGCGCGAAGTTTCGTTGCTACAA
ATGCTCTCCCACAGCATGTATATCGTCAGGCTACTTTGCGTGGAGCACGTCGAGAAA
GGCAGCAAGCCCATGCTCTACTTGGTCTTTGAATATATGGACACTGATCTTAAGAAG
TATATTGACTTGCACGGTCGTGGTCCGAGCGGGAAGCCTCTGCCTCCCAAAGTGGTC
CAGAGTTTCATGTATCAATTGTGCACAGGGCTTGCCCACTGTCATGGCCACGGAGTA
ATGCACAGGGATCTGAAACCCCAGAATTTGCTCGTCGACAAGCAAACCCGTCGTCTT
AAGATTGCCGACCTTGGTCTCGGTCGGGCATTCACAGTGCCAATGAAGAGTTACACA
CACGAGATTGTTACTCTATGGTACCGAGCTCCTGAAGTTCTTCTTGGAGCGACCCAC
TACTCTCTACCTGTGGATATCTGGTCTGTTGGGTGCATCTTCGCTGAACTCGTCCGGA
AAATGCCGCTCTTCACTGGAGACTCCGAACTTCAGCAGCTTCTTCACATCTTCAGGTT
GCTTGGCACCCCGAATGAGACAATCTGGCCTGGTGTTAGCCAGCACCGTGATTGGCA
CGAGTTTCCTCAATGGAGACCACAAGATCTGTCCCTTGCTGTTCCCGGACTCAGCGC
GGTTGGCTTAGACCTTCTCGCCAAAATGTTGGTATTCGAGCCCTCAAAGAGAATCTC
TGCCAAAGCCGCCTTGAGCCATACTTATTTCGCTGATGTTGATAAGACAGCAACCTA
AACACAACAGAACAATTCAAGAGAACCAGGTAACCTCTACCTGTCCAAGACGAAGG
TTAACGC

Nucleotide sequence of the full-length PK-8 from *Physcomitrella patens*

(SEQ ID NO: 16)

ATCCCGGGCAACGAGAAGCATTCGAGATGGCAGATGCGAAGGAGGAACTGGCGCTG
CGCACGGAAATGCACTGGGCTGTGAGGAGTAACGACGTGGGGCTGTTAAGGACCAT
TCTGAAGAAAGACAAGCAGCTCGTGAATGCTGCGGACTATGACAAGCGCACGCCCT
TGCACATCGCCGCGTCCCTGGATTGTGTCCCTGTTGCTAAAGTCCTGCTTGCGGAAG
GAGCAGAGTTGAATGCAAAAGACAGGTGGGGGAAATCTCCGAGAGGCGAGGCGGA
GAGTGCAGGATACATGGAGATGGTAAAGCTGTTGAAGGATTACGGGGCTGAGTCAC
ACGCAGGTGCCCCGAGGGGCCACGTTGAGAGTCTGATTCAGGTTGCCCCTCCGTTGC
CTTCTAACCGCGACTGGGAGATCGCTCCGTCGGAGATTGAACTTGATACCAGCGAGC
TCATCGGCAAAGGCGCCTTTGGAGAGATTCGGAAGGCGCTTTGGCGCGGCACACCC
GTCGCTGTGAAGACAATCAGACCTTCTCTGTCCAACGACAGAATGGTCATCAAGGAC
TTCCAGCACGAGGTGCAATTGCTCGTAAAGGTTCGGCACCCAAACATTGTGCAGTTC
CTCGGGGCTGTTACCCGTCAAAGACCTCTCATGTTAGTCACCGAGTTTCTGGCAGGG

APPENDIX-continued

GGCGATTTGCATCAGTTGCTGAGGAGCAACCCTAATTTGGCTCCTGACCGCATCGTG
AAGTATGCCCTCGACATAGCTCGCGGCATGTCTTACCTTCACAATCGGAGCAAGCCC
ATCATCCACCGCGATCTCAAACCCCGAAACATCATAGTGGACGAAGAGCATGAGCT
GAAGGTCGGCGACTTCGGACTGAGCAAGCTGATCGACGTAAAGCTTATGCATGATG
TGTACAAGATGACGGGGGGGACTGGGAGTTACAGATACATGGCGCCTGAGGTCTTC
GAACATCAACCCTACGACAAATCCGTCGACGTGTTTTCCTTTGGAATGATATTATAT
GAGATGTTTGAAGGCGTCGCTCCGTTTGAGGACAAGGATGCATACGACGCTGCCAC
ACTAGTTGCTAGAGACGATAAGCGGCCAGAGATGAGAGCCCAAACGTATCCCCCAC
AAATGAAGGCATTGATCGAGGATTGCTGGTCACCGTATACCCCGAAGCGACCACCTT
TCGTCGAAATCGTCAAAAAACTCGAGGTAATGTATGAGGATTGCTTATTGAGATTGC
CCAAAGACCGTCGTCATCTCCGCGACATCTTGCATCTTCGACGCAATCCTGCAGACT
CGTGATTGATCGGGCCAACCTTCGAGCTGATCAATCTAAGTAGTCAATGCCTTACTG
TGTCAAATTCAGCCTCCGCCGACAGATTGGCTATGGTTCAAGTGATTGGATTCTCTG
CTTCTCCAGAGCCAGAAACGACCCCCGTGCAATTTCTTCTCCGACGACCACATTGCG
ACATGAAGCACCAGACTTTGGATGTAGAAGGCATGGTCTACATGCTTTGCTGTGAGC
CTTGCACGTCTCGCAGGTTGATCTCTTTAACCAGCTTCTAGCCTTTCGCAATGGCTGC
ATCACTTAAGAAATCACCGAGTATCGTGATGCTCGTTAACGC

Nucleotide sequence of the full-length PK-9 from *Physcomitrella patens*

(SEQ ID NO: 17)

ATCCCGGGCTGTGATGTCGGTGTGGTGCTCTGCAAGAAATCAGATGACGTCATAAGC
ATGAAAAGGTACCAGAGACGTAAAGTTCAGAGACTCGOTCGGGAGGGCCAAGTCCT
ATTGGAGAGAACTCTTTTCAAGCAACTGAGGCCTTCCCCATTCGTGCCGCATCTCTT
GGCCACCCCTATTGACAGTGACAATGTGGCACTCGTTCTTAATTGTGTGTTAGCTGG
GCCTCTAGAACTTCTACTTCGGTCACCTTTAGACGAGAACTCAGCTCGTTTTCTGGTC
GCCAACGTGGTATTAGCCGTCGAACTTCTGCACAAGGATGGCGTTGTATATCGTGGC
ATCTCTCCCGATGTTCTTATGATAGATCGGAAAGGACGACTTCAGCTGGTTGATTTTC
GGTTTGCAAAGCAAATGTCGGATGAGCGCACTTTCACAGTCTGTGGCATGGCTGATT
TCTTAGCACCCGAGATCATTCAAGGACAAGGTCATGGCCTGGCTTCTGACTGGTGGG
CGGTAGGTGTGTTAATGTACTTCATGTTGCAAACTGAGCTTCCATTTGGATCATGGC
GGGACAACGAGCTTGAAATTTTTGGTAGAATAGCCCGTCGGCAGCTTACGTTTCCTT
CAAGTTTCAGCCCTGAAGCGGTTGACCTCATTGACAAGCTGCTGGTGGTGGACCCAA
CCAAGAGACTGGGCTGTGACAGCCATGGATCGCTTGCCATAAGGGAACATCCTTGG
TTCCGAGGTATAAACTGGGACAAGCACCTCGATTGCAGTGTGGAAGTTCCTTCAGAG
ATCATGACACGCCTTCAGTTGGCCATAGACTTTCTTCCCGTGGATGATAGTTATCAA
GTGTTTGATCTCCAACCCGATGAAGACGATCCACCATGGCTTGATGGCTGGTGATAG
CTTGATGGCTCGTAGATCCCCCTTCTCCAAGCATCAATGGCACAGTACCGAATGGCT
ATAACAGAAGATGCACATTAAGTGCTCCATGAACAGATACCGTAGCGCTTAGGATTT
TTCGGTCGTCACAAATGACGGCTCTCTTGTGAGGTTCGAATGTTGTGTCACCCGATG
ATCTCTACTGGCACAAACCTCCAGGCTGAATCTTAAGGCCAGCTGTTTTAGGTGAGA
CGTTTACCTTGGTTCGAACTCACGCTCGTGTTGTTAAGCGCGAGTCGATGATGTATG
AAATGACGGTGITCCTTGAAAGTCTTGAAAGGCAATCAATTCGCTTATGTGTGTCCC
TTCCATGTGGTCATTAGGGAAGGGAACCGCTGCACTAGTCAGTAAACGAACATGGC
TTCAATTGTATAGCATAGCGGTAGAGGTTTCGTACGAAATGTGGTTGCAGTCGGTGA
TTATAGGCGCATTTCTCTGAACATGCACGAGAATCGTGCTCCTGAGTCTCCATCATTC
AGTGGTGCGAGCTCGC

Nucleotide sequence of the full-length CK-1 from *Physcomitrella patens*

(SEQ ID NO: 18)

ATCCCGGGCTCACGTAGTGCACTGAACTCTGTCTGAATTTTAGGGGATGAGAGGTAG
ATTTGAAGAATACTGGTGTCTAATTTTCTGTTAATTTTTCACCCTTGAGGTAGCTCAT
GGATTTGGGAGGTGATCGCATGAGAGCTCCTCAGAGGCAGTCTCGAGAATATCAAT
ATAGATCATTGGACGTCTTCACAGAGCAGCACGAGCAGTTGCAAAAGCAGCAGCAG
CAAGATGAGTATCAGAGAACAGAATTGAAGCTCGAGACACTGCCAAAAATGTTAAG
CAATGCGACCGTGTCATCTTCCCCTCGAAGCAGTCCGGATGGACGTAGACTACGTAC
AGTCGCGAATAAGTATGCTGTGGAAGGTATGGTTGGGAGTGGCGCATTCTGCAAGG
TGTATCAGGGCTCCGATTTGACGAACCACGAGGTTGTGGGCATCAAGCTGGAGGAT
ACGAGAACTGAGCACGCTCAGTTAATGCACGAGTCGCGCTTGTACAACATATTGCG
GGGTGGGAAGGGAGTGCCCAACATGAGATGGTTCGGAAAAGAGCAAGACTACAAT
GTGATGGTGCTAGACCTATTGGGGCCGAACCTGTTGCACCTCTTTAAGGTGTGTGGG
CTAAGGTTTTCGTTGAAGACCGTGATTATGCTCGGTTACCAAATGATTGACCGGGTG
GAATACGTGCATTCTCGAGGGCTCGTTCACCGTGACCTGAAGCCGGATAACTTCCTC
ATGGGCTGCGGTCGGCAAGGAAACCAAGTGTTCATTATAGATTTTGGCTTGGCAAAG
GAGTACATGGACCCGGCAACACGAAGGCATATCCCTTACCGAGATAGGAAGAGCTT
CACAGGGACGGCACGGTACGCTAGTAGGAATCAGCACAGAGGAATCGAGCACAGT
AGAAGAGATGACATAGAATCACTTGGTTACATTCTTATGTACTTTCTAAGAGGCAAT
TTGCCATGGCAAGGGAAGGGCGGGCAACGCCTCACTGACCAGAAGCAACACGAGTA
CATGCACAACAAAATCAAGATGAACACCACTGTGGAGGAGCTTTGTGATGGGTATC
CCAGTCAATTTGCCGACTTTTTGCACCACGCGCGAAGTCTAGGTTTCTACGAGCAGC
CTGACTACTGTTACCTCCGAAGCTTGTTCCGTGATCTTTTCATTCAGAAAAAATTCCA
GCTCGACCATGTGTACGACTGGACTGTGTATACTCAACTCCCCCAGAATGGCTCTCT
GCAATCAGTGCGCAGCCAGAATTCCGCTGCTTCGTCCCATTTGCAAAATCGACCTTC
GAATGTATCATATTGTCCACCCTTGACCAAGTCGGAGTTCCGTCGTGAGGTTGTTGC
GGCGAATTAGGGCTTACGTTGGGAGGACTAGTGGTTCATCCTCTGCTCTGGTACTAA
AATAGCACAAGGTTGCTTACTGTTTCCCTCTCTCAAGTCTTACATGATTGTGAATGGG
GGTTTATGGAGTTGAGGATGAGGCAACTAAGCAGAGTGTAGGAAAAGAGTTGTAGA
CTCTCTAGTGTGTAGTGTGTAAATCAAGGCTTCTAGCATTGTGTCGGTAGCTTGTATG

APPENDIX-continued

GATCAGACTAGAAATGACTTTATCCATTACAAGAATTTTTACTCGGAAAGCCCATGA
CGGTGATGATTTCAATACGTTGCACAAGCAACTTTCTTCTGTAATTGAAATAGAGGA
TCTGGTCTGAGTATGAGAAGATGGGCATGTTAACGC

Nucleotide sequence of the full-length CK-2 from *Physcomitrella patens*

(SEQ ID NO: 19)

ATCCCGGGTTGTCGAGGACGGAGAGAGAAGAGAGAGAGAGAGAGAGAGGTG
TTGTTTAGGGGAGGCATGCGGGAGCAGGATTGGTGTTAAGTTCGTAAGGAGAAGGG
AGTACATGCAAGTGCGTGCTTGTCGGATATCGGACAGCTGGATTTGTAAATAAGCGG
AGAGGAGGGTCGGTAATCAGGGGCGTACATCGATGGAGCCGCGTGTGGGAAACAAG
TATCGGCTGGGACGGAAAATTGGGAGCGGTTCCTTTGGGGAGATCTATCTTGGGACC
AATGTTCAGACCAATGAGGAGGTCGGAATAAAGCTGGAAAGCATCAAGACGAAGCA
TCCACAATTGCTGTACGAGTCCAAGCTCTACCGGATACTACAAGGAGGAACTGGGA
TTCCCAATATCAGATGGTTCGGGATAGAAGGAGACTACAATGTCTTGGTTCTGGATC
TGTTGGGGCCAAGTCTCGAAGACCTTTTCAACTTCTGCAGCCGGAAGTTCTCTTTAA
AGACTGTTCTCATGCTTGCTGACCAGCTGATCAACAGAGTGGAGTATGTGCATGCGA
AAAGCTTTCTTCATAGAGACATCAAGCCTGATAATTTTCTAATGGGGCTTGGTAGGC
GAGCAAACCAGGTCTACATTATTGATTTTGGTCTTGCCAAGAAGTACCGCGACCCTT
CCACGCATCAGCATATTCCCTACAGGGAGAACAAAAATCTGACAGGGACTGCTCGG
TATGCAAGCATCAACACTCATCTTGGTATTGAGCAAAGCAGACGAGATGATTTGGAA
TCTCTTGGATATGTGCTCATGTACTTCCTGAGAGGCAGTCTTCCATGGCAAGGACTG
AAAGCGGGAACCAAGAAGCAGAAGTACGAGAAGATCAGTGAGAAAAAAATGTCCA
CGCCCATTGAGGTCCTTTGTAAAAATTATCCTTCAGAATTCGCCTCGTACTTCCACTA
CTGCCGGTCCTTGCGTTTTGATGACAAACCCGACTATGCATATTTGAAAAGAATCTT
CCGTGACCTCTTTATTCGTGAGGGTTTTCAATTTGACTACGTTTTTGACTGGACAATT
CTGAAGTACCAGCAGTCACAAATTTCCGGTGGCAGTTCAACTCGACTGGGTGCTTCT
GCAGGGCAAACCAGTGGTGCACTTGGAACTGGGGCTACAGGAAGCCGAGACCTGCA
GCGGCCCACCGAACCAATGGATCCTTCTCGGCGCAGGCTTCCTGGAGGAGCAAATG
GCTCCGGGGTCGCAAATGCTTTGGACTCATCTAAGCACAAAAGTCCTGGACTTGATG
AATCTGCTAAGGATTCTGCTCTTGCTGTTGTGTCAGAACCAGAGCGCATGCATACAT
CTTCGTATGCAACTCGGGGGGGTTCTTCCTCCAGGCGAGCTGTCCTATCTAGCAGCA
GGCCCTCAGGGGCATCAGCAGAAGTCGTAGATTCCTCTCGAACAGGGAGCAGTAAG
CTTGGTCCCACCAGCTTACGGTCGTCAGCAGGGATGCAGAGGAGCTCTCCAGTTACT
TCGGACCCAAAGCGGATATCTAGCCGCCATCCACAACCGCCATCTGCCAACTTGAGG
ATTTACGAAGCCGCTATCAAGGGAGTTGAATCACTTTCTGTTGAGGTGGATCAAAGC
CGTTATAAGTAGGCCCAGGCTTGTGGTTATATAGCCGGGCTCTGTCTTCTATCAAAC
CCTCTTGTTATGTAGATGAGAGTTGCTCTACATTTGGCAACAGCCTGATTGAGGGGA
AAACGGTGGTTCTGTCCTACAATGGTGCTAAGACTACAGGTCTCTCATACTTAGGAA
TGAATGGATCTCTATCTTGTTACCATCAAACCATTGTCAGTGCTTTGTGTGGTAGCTC
TCTGCCATACGATTCCTAAGGTTAACGC

Nucleotide sequence of the full-length CK-3 from *Physcomitrella patens*

(SEQ ID NO: 20)

GCGTTAACGGGAGGAAGGTCGGGGGAAGAGACGCTTGAGGCTGCTGAAAGGGGATT
CACTCAGCGTCCCCACCCATTCGTCAATCTGGCGCAGAAGATCGGAAAATCGGTCCG
ACGGCCAGGTGTTATGTCCAAGGCCCGGGTTTACACAGATGTGAATGTCCAACGTCC
GAAAGATTATTGGGACTACGAGGCCCTCACCGTCCAATGGGGGGACCAAGACGATT
ACGAGGTAGTGCGTAAGGTGGGGCGAGGGAAATACAGTGAGGTTTTTGAAGGTGTC
AACGCCGTGAATAGTGAGCGTTGCGTTATGAAGATTTTGAAGCCAGTAAAGAAAAA
AAAGATCAAAAGAGAGATCAAGATTCTGCAAAACCTTTGTGGAGGGCCCAACATTG
TGAAGCTTCTGGACATTGTCCGTGATCAGCAATCGAAGACACCCAGCCTAATTTTTG
AGTATGTGAACAATACTGATTTCAAAGTGCTCTACCCCACTCTTACAGACTTTGATA
TCCGATACTACATTCATGAGCTGCTCAAGGCTTTGGACTATTGCCATTCTCAAGGGA
TTATGCACAGGGATGTGAAGCCACACAACGTGATGATTGACCATGAGCAGCGGAAG
CTTAGGCTTATTGACTGGGGACTTGCCGAATTCTATCATCCTGGCAAAGAGTATAAT
GTGCGTGTTGCCTCTAGGTACTTCAAGGGTCCTGAGCTGCTGGTTGATCTTCAAGATT
ATGATTACTCTCTCGACATGTGGAGCTTGGGGTGCATGTTTGCCGGCATGATATTTC
GGAAGGAGCCATTCTTTTATGGGCATGACAATTATGATCAACTTGTGAAGATTGCTA
AGGTGTTGGGAACTGATGAATTGAATTCCTATCTAAACAAATACCGCCTAGAGCTGG
ACCCCCATTTGGAAGCACTGGTTGGCAGGCATAGCAGGAAACCTTGGTCAAAGTTC
ATCAATGCTGATAATCAGCGTCTGGTTGTTCCAGAGGCTGTGGATTTTTTGGATAAG
CTTCTACGCTACGATCATCAAGACAGGCTGACTGCGAAGGAAGCTATGGCACATCCC
TATTTTTATCCCGTGAAGGTGTCGGAGGTTAGCAACCGTCGCAGTGCTTGATATGAA
TTGATATATCTCATATGGGCTTTCTTGTGATTACGTCCCACCCGGCTACCAGGTTTCT
CAGTTGTGCGAAGCGCTGAGCTCGC

Nucleotide sequence of full-length MPK-2 from *Physcomitrella patens*

(SEQ ID NO: 21)

ATCCCGGGCGAGCCATGGCGCCACTTGCTTCGGCGAATGGGACTGTTTGACTTCTTC
GCTTCGCCCCCGCCTCGCCCTTCACCCTCCTCTGTTCTTGTCACAGCCTCCTCCTCCG
TCTCTGTCTGTTGGCTGGGTAAGTTTTGGGAGTGAGGAGGACGTGGTCATGGAAGAA
GAGCCCCCCTCTTTTGTAGTGGACTGTCGGTAAATTGGACCTGGAGCCTGCCGGCTC
ATCGCGTTTGCTTAGATTGTGGGCGGGTGCTGTTGAAATTCCTTGAACTTGCTACTGG
TCGGAAACGCTCGAATTGCGACTTTGATTGAAGGTCTGGTTGTTGCTGCGGTCGGGA
TCTTACTCAGTCTCTTCAATAGGACCTCTGAAGCAGTATGGAGACTAGCAGTGGAAC
TCCAGAATTGAAAGTTATAAGTACTCCGACCTACGGAGGTCATTACGTGAAATATGT
TGTGGCGGGAACTGATTTCGAAGTCACCGCGAGGTACAAGCCACCACTTCGTCCGAT

APPENDIX-continued

TGGGCGCGGAGCTTATGGAATCGTCTGTTCACTCTTTGATACCGTTACGGGTGAGGA
GGTGGCGGTCAAAAAGATTGGAAACGCCTTCGACAACAGGATCGATGCGAAGCGAA
CACTGCGTGAAATAAAACTCCTCCGGCATATGGATCATGAAAACGTCGTTGCCATTA
CAGACATCATTCGTCCCCCAACTAGGGAGAATTTCAACGACGTGTACATTGTATACG
AGTTGATGGATACGGACCTACACCAGATCATTCGTTCAAATCAAGCTCTCACAGAAG
ACCACTGTCAGTATTTTCTGTATCAAATCTTGCGGGGCTTGAAGTACATCCATTCGGC
GAACGTCTTGCACCGGGACTTGAAGCCCACCAACCTTCTCGTCAATGCCAATTGCGA
TTTGAAAATCGCAGATTTTGGCTTGGCACGCACTCTCTCTGAAACGGATTTCATGAC
TGAGTATGTTGTAACGAGGTGGTACAGAGCTCCAGAGCTGCTCCTGAATTGTTCAGC
ATACACTGCAGCTATTGACATTTGGTCTGTGGGGTGCATCTTCATGGAGTTGCTTAA
CCGATCTGCGTTGTTCCCTGGGAGAGACTATGTGCATCAGCTCCGCCTAATTACAGA
ACTCATCGGAACTCCTGAAGATAGGGATCTTGGGTTTTTGAGAAGCGACAATGCTAG
GCGGTATATCAAGCACCTGCCTCGACAGTCGCCTATTCCCTTAACCCAGAAGTTCAG
AGGCATTAATCGTTCTGCTCTTGATCTTGTTGAAAAGATGCTGGTCTTTGATCCAGCG
AAAAGAATCACAGTGGAAGCTGCCTTGGCGCACCCTTATTTAGCTTCACTTCATGAC
ATCAACGATGAGCCTGCCTCGGTATCTCCCTTCGAGTTTGACTTCGAGGAGCCCCCT
ATCTCGGAGGAGCATATCAAGGATCTCATTTGGAGGGAGGCTCTGGATTGCAGCTTA
GGTCCTGATGATATGGTGCAGTAACTTCACACTTCATCTCAAGTTGTAAGGCCTACT
CTCAATTCTTTAGGTGGCTACAACGCTATCCCGGCGTTGTATGGTTTTGCAACTTATT
CCCCCCCGTGTGATTACACTATTGGATTATAGAATGACAATTCGTTAGTTCTTTTCCC
TGGCGCTATATCTTTGTCTGCACATTTCATCCAGCAGACATTGTTGCTCGGCGTTAAC
GC

Nucleotide sequence of full-length MPK-3 from *Physcomitrella patens*

(SEQ ID NO: 22)

ATCCCGGGCTTGTATTGGCTCGGATAATTTATGTTGACAATTGATTTGTGAGGCTTCG
TATTGAGTCAGCGAGCAGGCTGAGAGTTCGGCAGCGAAGTTACACTCGACCTGGCT
GAAATTTGGAATTGAAGCGCGTGAAGCTTCATCTGTGATTTTGGAGGTTGTTTGACT
GATGAGAAGAGGTCTCTGAGCTGAGAATGTTTGCAATTTAGGGGCACCACCGGTTTG
TTGGAGTCCCTTGCCACTTATTACAATTGTTGGTTTACAAGCTCGACGAGTTTCAATC
GAACGTAGAGTTTTAGTCGGGTCGAGGATCTATGTATCCGCTCAGCGGAGAAGAGA
GCCTGATGTTGCCGAAGCGATCGTGTGGGATTTGACTAGAAAGAGGTGGACCGCAT
CAGAACTATTTATTCCTTGTGAGGGAAGGATCGAGGTTCCAATGGGTCTCACTCCGT
TTTCTTGTGTCACGGTTCAAGGTTATGTCCGGGTGGTCTACCCCGACGGCCACGTCG
AGAATCTGAGCAAATCTTGTAGCGTGCACGATCTTCTTCTGGGTAATCCAGACTACT
ATGTCTGCGGTAGCACCCCTTACACAATCACCAATCGTATGGCAGCGGAAGAGGTG
CTCGAGTATGGGGTGACCTACTTCGTTTGCGCAACGCCAAATGCCCAACCTTTCTTA
GAACGTCAGCCGAAGGTAGTACATCGAGGATCCAAGATTTTGCCACGATTTTCCAAA
CATGGGGTCCATGTGCGGGAGTTGCGAAGCCCGACGCATGGGAGCCAACAGTCACG
GAAGGTTTTTGATTATCATTCAGTAACGATGCAGCAGCTTGAATCCATACGAAACGA
GGGCCCAGAGCCTCACCTCGCTGGAGACCGACCATCGAAGCACCTTAAGCTCGTTTT
CATTCGGCATTGCTTGCGAGCACTTCGACTTCCTAGAATTTCAATAGACCTAATGGA
ATCGCCACTCCCTAATCTTTCCGGAGAGGCCTTATCGCCGACGGCAACTGCCAAAGA
CGAGATTACTCAGATGATACTAAAAAGTGCCGCAAGGTCCGAATTAGGAATGTATG
TTTCGAAGAGACAGGAATTCTATCTTCGAAGAGCGCGTAGGCGGCGTAAGTTTGCGT
GGAAGCCGGTTTTGCAGAGCATCTCCGAGATGAAGCCTGTCATGGAATTCCACACTC
CGATGGCTTACCGGGATAGTGGGTCTCCGCCGAAGAACGCCTCTACCCCATCCTTAC
CTGGCCCGAAGAACATTTCACCGCCACGACAAGTGAGTGTCCCGCAAAGGAGCAGT
CCTCCGCCGAAGAACGTCTCACCACCTCCCCAGCCCGCATTTGTAGCGCGGACTGCG
TCGAAGTATTCTGCTGCATCTCAGCAAGTTCAACGAAATCGAGGCAACGCGAAATCT
CTTTATATGGCGTAGTTTGTGTCTCGACTGAACTCCTATCTATTCCCCCATCGAGATA
ACTGCATTCGTTGGATAAATTTCTCCAACATTTTTGCTCTTCATCCTCAAGCAGCTCC
TCAATGGCCAGTAATATGTTACGACATTGTGCACAACTCCAATTACGTAGCGTTATT
CTGTAACCCACGTTCATCGAGGTATCAAGGAATGGCGCAGTAAGCACTGCTACTTTG
TGCTTTGGTATCCCGTTGTGACGAGATGTCATGTCGCACCGTGCCTATCAGTGGGAT
TTTCTTGAGCGCAGATCTTGCTTCCGCAGTTTGTTTCATAACGTTTTGGTTCGTAGGG
GGCCTAGACGGTACTATCAAGCAATGAGAAGTGTGCTGGTGTGGATTTGACAGCAA
TCTTTTGGAGGATTGTCTTTCCTATGTAGAACATAGCGAGGACACTTGCGCCTGGTG
GGCACATCCCATAGAACATAGTGCTTCACTTCTGGGTTGTTCACCACTAGGATCATA
TGACCTTCTCATCTATTTTCGGGCTTTGTTTCGAGCTCATGTACCATCGACTAGCGTC
ACTTTGACTGCGGTGATAATCGTTTGTCAATTTAGTGGAGCTTTGTAGATGATAGAT
GCCATTTGTACAGTAGCTTGGATGCTGTTTACAAGATAGCGGCAGCTAGAAGCCTTA
AACCTTTAGCTACCATGTATTATTTAAACCTATATGAAGTGAACGGCTGTGCAGATA
TTGCCGTTAACGC

Nucleotide sequence of full-length MPK-4 from *Physcomitrella patens*

(SEQ ID NO: 23)

ATCCCGGGCGGTCGAGTCGTATTAGGTGTTGTTTCATTGTAAGGGTTCGGAAGCACG
GGGCACGGCGTATATACCGTTCCCCTTGAACGTTGATCTCACCTTTGGAAGACCTGA
ATTGAGTAGCGTGCGGAAGCTGCATCGATCCGGAAGAGACGATGAGTAGGAGAGTG
AGAAGGGGAGGTCTTCGCGTCGCGGTGCCGAAGCAAGAGACTCCCGTCAGCAAATT
TTTGACTGCCAGTGGAACTTTCCAGGATGATGATATCAAGCTCAACCACACCGGGCT
TCGCGTCGTCTCTTCAGAACCTAACCTTCCTACGCAGACGCAGTCTAGCTCCCCAGA
TGGGCAACTGTCAATAGCAGACCTGGAGTTAGTGCGGTTCTTGGGAAAGGGTGCGG
GTGGAACCGTGCAGCTTGTCCGGCACAAATGGACCAATGTCAATTATGCACTGAAG
GCGATACAAATGAATATCAACGAAACAGTGAGGAAGCAGATTGTTCAGGAGCTGAA
AATCAACCAAGTGACGCACCAGCAGTGCCCTTATATCGTGGAATGCTTCCACTCCTT
CTACCACAACGGCGTCATATCCATGATCCTAGAGTACATGGACAGGGGCTCGTTGTC

APPENDIX-continued

CGACATTATTAAGCAACAAAAGCAGATACCTGAGCCGTATTTGGCCGTCATTGCTAG
TCAAGTTCTGAAGGGATTGGAATACCTACACCAAGTCAGGCACATCATACATCGTGA
TATAAAGCCCTCCAACCTCCTCATCAATCACAAGGGTGAGGTCAAAATATCTGATTT
TGGTGTCAGTGCTGTGTTGGTTCATTCCTTGGCCCAGCGAGACACGTTCGTTGGGAC
TTGCACATATATGTCGCCAGAACGCCTTCAGGGGCGTTCGTATGCATACGACAGTGA
CCTATGGAGTTTAGGATTGACTCTTTTGGAGTGTGCGTTGGGTACCTTCCCATACAA
ACCAGCTGGAATGGAAGAGGOTTGGCAAAATTTCTTCATCCTCATGGAATGTATAGT
TAATCAACCCCCCGCAGCCGCATCCCCTGACAAATTCTCCCCCGAATTTTGTTCTTTT
ATTGAATCCTGCATCCGGAAATGTCCCAGTGAACGACCATCAACTACTGATTTACTT
AAACATCCGTTCCTGCAAAAGTACAACGAGGAAGAGTACCATTTGAGCAAGATTTT
GTAACTTAAAGTTAGCCTCGCATGGCGTGCAGAGACTGTCACTACCACAAGCCTGAT
CCACCACTGAACTTCAAGGGACTTTACCAAAAGCATGGTCGAACTACCTCGCCAATC
CGCCACTTTCTCAATGCCTTTTCCTTATATAGTCATATGTGGTCAAGTTGAGAACGAT
ATCAAATCAGATTGACGGAAAAAACATCTTCAACGCCGTTTCCCAACCTTATAGAAA
GTGGAGTTTTCTCAATGAGCCCCATTTGTCGCTGAGAACGTGCAGCTCATGAAACAA
TCCATAAGTGTGTTAATCGGGGTCTTATATTATCATCACCATGCTAGCTTTTTATGTT
ACCTGCACTTTTTCTTTCCTTATTGCACAGCATCGAACACTTCTTCGATACCCAAAAC
AATATTTCCATCTTCTTTCTTCTTTTTTTCACGTCTTGCGACAAGGAATTTCCTCACGG
AGATTTTTCAACACTTTTCTCAAATGTTTTTAGAGTTTTTAAACTGACAATTGAAGAG
GTCGGACCTACCGGACTCGC

Nucleotide sequence of full-length MPK-5 from *Physcomitrella patens*

(SEQ ID NO: 24)

ATCCCGGGAGAGGCTGATCTGATGCTACAGTTTCGTGTGCAGCTAGTCTTTAGAGAT
TCGGGCAACGCACTTGTTGAAGATCGGAAACTTTCAAAATCGGTCGAGTCGTATTAG
GTGTTGTTTCATTGTAAGGGTTCGGAAGCACGGGGCACGGCGTATATACCGTTCCCC
TTGAACGTTGATCTCACCTTTGGAAGACCTGAATTGAGTAGCGTGCGGAAGCTGCAT
CGATCCGGAAGAGACGATGAGTAGGAGAGTGAGAAGGGGAGGTCTTCGCGTCGCGG
TGCCGAAGCAAGAGACTCCCGTCAGCAAATTTTTGACTGCCAGTGGAACTTTCCAGG
ATGATGATATCAAGCTCAACCACACCGGGCTTCGCGTCGTCTCTTCAGAACCTAACC
TTCCTACGCAGACGCAGTCTAGCTCCCCAGATGGGCAACTGTCAATAGCAGACCTGG
AGTTAGTGCGGTTCTTAGGAAAGGGTGCGGGTGGAACCGTGCAGCTTGTCCGGCAC
AAATGGACCAATGTCAATTATGCACTGAAGGCGATACAAATGAATATCAACGAAAC
AGTGAGGAAGCAGATTGTTCAGGAGCTGAAAATCAACCAAGTGACGCACCAGCAGT
GCCCTTATATCGTGGAATGCTTCCACTCCTTCTACCACAACGGCGTCATATCCATGAT
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Nucleotide sequence of full-length CPK-1 from *Physcomitrella patens*

(SEQ ID NO: 25)

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APPENDIX-continued

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Nucleotide sequence of full-length CPK-2 from *Physcomitrella patens*

(SEQ ID NO: 26)

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Deduced amino acid sequence of PK-6 from *Physcomitrella patens*

(SEQ ID NO: 27)

MGVDMKAPAKQSLGVGLLLCSVVILSVVSSVYGQVQTDPVDTTGLISMWYDLKQSQSL
TGWTQNASNPCGQQWYGVVCDGSSVTEIKIGSRGLNGNFNPSYFQNAFKKLRIFDASNN
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VNKSNIAATPFSVADLQAATNSFSQDNLIGEGSMGRVYRAEFPNGQVLAVKKIDSSASM
VQNEDDFLSVVDSLARLQHANTAELVGYCIEHDQRLLVYEYVSRGTLNELLHFSGENTK
ALSWNVRIKIALGSARALEYLHEVCAPPVVHHNFKSANILLDDELNPHVSDCGLAALAPS
GSERQVSAQMLGSFGYSAPEYAMSGTYTVKSDVYSFGVVMLELLTGRKSLDSSRPRSEQ
SLVRWATPQLHDIDALARMVDPSLKGIYPAKSLSRFADIVALCVQPEPEFRPPMSEVVQA
LVRLMQRASLSKRRSESAVGIESNEPSETSL

Deduced amino acid sequence of PK-7 from *Physcomitrella patens*

(SEQ ID NO: 28)

MSVSGMDNYEKLEKVGEGTYGKVYKARDKRSGQLVALKKTRLEMEEEGVPSTALREV
SLLQMLSHSMYIVRLLCVEHVEKGSKPMLYLVFEYMDTDLKKYIDLHGRGPSGKPLPPK

APPENDIX-continued

VVQSFMYQLCTGLAHCHGHGVMHRDLKPQNLLVDKQTRRLKIADLGLGRAFTVPMKS
YTHEIVTLWYRAPEVLLGATHYSLPVDIWSVGCIFAELVRKMPLFTGDSELQQLLHIFRLL
GTPNETIWPGVSQHRDWHEFPQWRPQDLSLAVPGLSAVGLDLLAKMLVFEPSKRISAKA
ALSHTYFADVDKTAT

Deduced amino acid sequence of PK-8 from *Physcomitrella patens*

(SEQ ID NO: 29)

MADAKEELALRTEMHWAVRSNDVGLLRTILKKDKQLVNAADYDKRTPLHIAASLDCVP
VAKVLLAEGAELNAKDRWGKSPRGEAESAGYMEMVKLLKDYGAESHAGAPRGHVESL
IQVAPPLPSNRDWEIAPSEIELDTSELIGKGAFGEIRKALWRGTPVAVKTIRPSLSNDRMVI
KDFQHEVQLLVKVRHPNIVQFLGAVTRQRPLMLVTEFLAGGDLHQLLRSNPNLAPDRIV
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TGGTGSYRYMAPEVFEHQPYDKSVDVFSFGMILYEMFEGVAPFEDKDAYDAATLVARD
DKRPEMRAQTYPPQMKALIEDCWSPYTPKRPPFVEIVKKLEVMYEDCLLRLPKDRRHLR
DILHLRRNPADS

Deduced amino acid sequence of PK-9 from *Physcomitrella patens*

(SEQ ID NO: 30)

MKRYQRRKVQRLGREGQVLLERTLFKQLRPSPFVPHLLATPIDSDNVALVLNCVLAGPL
ELLLRSPLDENSARFLVANVVLAVELLHKDGVVYRGISPDVLMIDRKGRLQLVDFRFAK
QMSDERTFTVCGMADFLAPEIIQGQGHGLASDWWAVGVLMYFMLQTELPFGSWRDNE
LEIFGRIARRQLTFPSSFSPEAVDLIDKLLVVDPTKRLGCDSHGSLAIREHPWFRGINWDK
HLDCSVEVPSEIMTRLQLAIDFLPVDDSYQVFDLQPDEDDPPWLDGW

Deduced amino acid sequence of CK-1 from *Physcomitrella patens*

(SEQ ID NO: 31)

MDLGGDRMRAPQRQSREYQYRSLDVFTEQHEQLQKQQQQDEYQRTELKLETLPKMLS
NATVSSSPRSSPDGRRLRTVANKYAVEGMVGSGAFCKVYQGSDLTNHEVVGIKLEDTR
TEHAQLMHESRLYNILRGGKGVPNMRWFGKEQDYNVMVLDLLGPNLLHLFKVCGLRFS
LKTVIMLGYQMIDRVEYVHSRGLVHRDLKPDNFLMGCGRQGNQVFIIDFGLAKEYMDP
ATRRHIPYRDRKSFTGTARYASRNQHRGIEHSRRDDIESLGYILMYFLRGNLPWQGKGG
QRLTDQKQHEYMHNKIKMNTTVEELCDGYPSQFADFLHHARSLGFYEQPDYCYLRSLF
RDLFIQKKFQLDHVYDWTVYTQLPQNGSLQSVRSQNSAASSHLQNRPSNVSYCPPLTKS
EFRREVVAAN

Deduced amino acid sequence of CK-2 from *Physcomitrella patens*

(SEQ ID NO: 32)

MEPRVGNKYRLGRKIGSGSFGEIYLGTNVQTNEEVGIKLESIKTKHPQLLYESKLYRILQG
GTGIPNIRWFGIEGDYNVLVLDLLGPSLEDLFNFCSRKFSLKTVLMLADQLINRVEYVHA
KSFLHRDIKPDNFLMGLGRRANQVYIIDFGLAKKYRDPSTHQHIPYRENKNLTGTARYAS
INTHLGIEQSRRDDLESLGYVLMYFLRGSLPWQGLKAGTKKQKYEKISEKKMSTPIEVLC
KNYPSEFASYFHYCRSLRFDDKPDYAYLKRIFRDLFIREGFQFDYVFDWTILKYQQSQISG
GSSTRLGASAGQTSGALGTGATGSRDLQRPTEPMDPSRRRLPGGANGSGVANALDSSKH
KSPGLDESAKDSALAVVSEPERMHTSSYATRGGSSSRRAVLSSSRPSGASAEVVDSSRTG
SSKLGPTSLRSSAGMQRSSPVTSDPKRISSRHPQPPSANLRIYEAAIKGVESLSVEVDQSR
YK

Deduced ammo acid sequence of CK-3 from *Physcomitrella patens*

(SEQ ID NO: 33)

MSKARVYTDVNVQRPKDYWDYEALTVQWGDQDDYEVVRKVGRGKYSEVFEGVNAV
NSERCVMKILKPVKKKKIKREIKILQNLCGGPNIVKLLDIVRDQQSKTPSLIFEYVNNTDF
KVLYPTLTDFDIRYYIHELLKALDYCHSQGIMHRDVKPHNVMIDHEQRKLRLIDWGLAE
FYHPGKEYNVRVASRYFKGPELLVDLQDYDYSLDMWSLGCMFAGMIFRKEPFFYGHDN
YDQLVKIAKVLGTDELNSYLNKYRLELDPHLEALVGRHSRKPWSKFINADNQRLVVPEA
VDFLDKLLRYDHQDRLTAKEAMAHPYFYPVKVSEVSNRRSA

Deduced amino acid sequence of MPK-2 from *Physcomitrella patens*

(SEQ ID NO: 34)

METSSGTPELKVISTPTYGGHYVKYVVAGTDFEVTARYKPPLRPIGRGAYGIVCSLFDTV
TGEEVAVKKIGNAFDNRIDAKRTLREIKLLRHMDHENVVAITDIIRPPTRENFNDVYIVYE
LMDTDLHQIIRSNQALTEDHCQYFLYQILRGLKYIHSANVLHRDLKPTNLLVNANCDLKI
ADFGLARTLSETDFMTEYVVTRWYRAPELLLNCSAYTAAIDIWSVGCIFMELLNRSALFP
GRDYVHQLRLITELIGTPEDRDLGFLRSDNARRYIKHLPRQSPIPLTQKFRGINRSALDLVE
KMLVFDPAKRITVEAALAHPYLASLHDINDEPASVSPFEFDFEEPPISEEHIKDLIWREALD
CSLGPDDMVQ

Deduced amino acid sequence of MPK-3 from *Physcomitrella patens*

(SEQ ID NO: 35)

MGLTPFSCVTVQGYVRVVYPDGHVENLSKSCSVHDLLLGNPDYYVCGSTPYTITNRMA
AEEVLEYGVTYFVCATPNAQPFLERQPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQS
RKVFDYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIRHCLRALRLPRISIDLMESPL

APPENDIX-continued

PNLSGEALSPTATAKDEITQMILKSAABSELGMYVSKRQEFYLRRARRRRKFAWKPVLQ
SISEMKPVMEFHTPMAYRDSGSPPKNASTPSLPGPKNISPPRQVSVPQRSSPPPKNVSPPP
QPAFVARTASKYSAASQQVQRNRGNAKSLYMA

Deduced amino acid sequence of MPK-4 from *Physcomitrella patens*

(SEQ ID NO: 36)

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PDGQLSIADLELVRFLGKGAGGTVQLVRHKWTNVNYALKAIQMNINETVRKQIVQELKI
NQVTHQQCPYIVECFHSFYHNGVISMILEYMDRGSLSDIIKQQKQIPEPYLAVIASQVLKG
LEYLHQVRHIIHRDIKPSNLLINHKGEVKISDFGVSAVLVHSLAQRDTFVGTCTYMSPERL
QGRSYAYDSDLWSLGLTLLECALGTFPYKPAGMEEGWQNFFILMECIVNQPPAAASPDK
FSPEFCSFIESCIRKCPSERPSTTDLLKHPFLQKYNEEEYHLSKIL

Deduced amino acid sequence of MPK-5 from *Physcomitrella patens*

(SEQ ID NO: 37)

MSRRVRRGGLRVAVPKQETPVSKFLTASGTFQDDDIKLNHTGLRVVSSEPNLPTQTQSSS
PDGQLSIADLELVRFLGKGAGGTVQLVRHKWTNVNYALKAIQMNINETVRKQIVQELKI
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QGRSYAYDSDLWSLGLTLLECALGTFPYKPAGMEEGWQNFFILMECIVNQPPAAASPDK
FSPEFCSFIESCIRKCPSERPSTTDLLKHPFLQKYNEEEYHLSKIL

Deduced amino acid sequence of CPK-1 from *Physcomitrella patens*

(SEQ ID NO: 38)

MGQCYGKFDDGGEGEDLFERQKVQVSRTPKHGSWSNSNRGSFNNGGGASPMRAKTSF
GSSHPSPRHPSASPLPHYTSSPAPSTPRRNIFKRPFPPPSPAKHIQSSLVKRHGAKPKEGGAI
PEAVDGEKPLDKHFGYHKNFATKYELGHEVGRGHFGHTCYAKVRKGEHKGQAVAVKII
SKAKMTTAIAIEDVGREVKILKALTGHQNLVRFYDSCEDHLNVYIVMELCEGGELLDRIL
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KNSTEAMKESRVFEILESMDGLHFKKMDFSEFCAAAISVLQLEATERWEQHARAAYDIF
EKEGNRVIYPDELAKEMGLAPNVPAQVFLDWIRQSDGRLSFTGFTKLLHGISSRAIKNLQ
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Deduced amino acid sequence of CPK-2 from *Physcomitrella patens*

(SEQ ID NO: 39)

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AETEQGIFDAVLKGHIDFENDPWPKISNGAKDLVRKMLNPNVKIRLTAQQVLNHPWMK
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tgaagtcgtc ctttccgatc tatcataaga acatcgggag agatgccacg atatacaacg 360

ccatccttgt gcagaagttc gacggctaat accacgttgg cgaccagaaa acgagctgag 420

ttctcgtcta aaggtgaccg aagtagaagt tctagaggcc cagctaacac acaattaaga 480

acgagtgcca cattgtcact gtcaataggg gtggccaaga gatgcggcac gaatggggaa 540

ggcctcagtt gcttgaaaag agttctctcc aataggactt ggccctcccg accgagtctc 600

tgaactttac gtctctggta ccttttcatg cttatgacgt catctgattt cttgcagagc 660

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<210> SEQ ID NO 5
<211> LENGTH: 1271
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (619)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 5

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ataaagtcat ttctagtctg atccatacaa gctaccgaca caatgctaga agccttgatt 180

tacacactac acactagaga gtctacaact cttttcctac actctgctta gttgcctcat 240

cctcaactcc ataaaccccc attcacaatc atgtaagact tgagagaggg aaacagtaag 300

caaccttgtg ctattttagt accagagcag aggatgaacc actagtcctc ccaacgtaag 360

ccctaattcg ccgcaacaac ctcacgacgg aactccgact tggtcaaggg tggacaatat 420

gatacattcg aaggtcgatt ttgcaaatgg gacgaagcag cggaattctg gctgcgcact 480

gattgcagag agccattctg ggggagttga gtatacacag tccagtcgta cacatggtcg 540

agctggaatt ttttctgaat gaaaagatca cggaacaagc ttcggaggta cagtagtcag 600

gctgctcgta aaaacctana cttcgcggcg tggtgcaaaa agtcggcaaa ttgactggga 660

tacccatcac aaagctcctc ccacagtggg ggtcatcttg attttgttgt gcatgtactc 720

gtgttgcttc tggtcagtga gggcgttgcc cgcccttccc ttgccatggc aaattgcctc 780

ttagaaagta cataagaatg taacccaagt gattctatgt catctcttct actgtgctcg 840

attcctctgt gctgattcct actagcgtac cgtgccgtcc ctgtgaagct cttcctatct 900

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cggtaaggga tatgccttcg tgttgccggg tccatgtact cctttgccaa gccaaaatct 960

ataatgaaca cttggtttcc ttgccgaccg cagcccatga ggaagttatc cggcttcagg 1020

tcacggtgaa cgagccctcg agaatgcacg tattccaccc ggtcaatcat ttggtaaccg 1080

agcataatca cggtcttcaa cgaaaacctt agcccacaca ccttaaagag gtgcaacagg 1140

ttcggcccca ataggtctag caccatcaca ttgtagtctt ctgctgcttt tccgaaccat 1200

ctcatgttgg gcactccctt cccaccccgc aatatgttgt acaagcgcga ctcgtgcatt 1260

aactctcgtg c 1271

<210> SEQ ID NO 6
<211> LENGTH: 1910
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 6

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aacaagctaa tggctgcaag cagtgaacat actaccaagg gagagattct cactccctag 120

acttcatcct cgtacgttac ttggcaagga ttatggttta gtgataaaaa gcttcacaag 180

ccggcaagca tgctggttgc ttctgctgca atctaatgat tatttcctta ggaatcgtat 240

ggcagagagc taccacacaa agcactgaca atggtttgat ggtaacaaga tagagatcca 300

ttcattccta agtatgagag acctgtagtc ttagcaccat tgtaggacag aaccaccgtt 360

ttcccctcaa tcaggctgtt gccaaatgta gagcaactct catcaacata acaagagggt 420

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tggatccacc tcaacagaaa gtgattcaac tcccttgata ccggctttcg taaatcctca 540

agttggcaga tggcggttgt ggatggcggc tagatatccg ctttgggtcc gaagtaactg 600

gagagctcct ctgcatccct gctgacgacc gtaagctggt gggaccaagc ttactgctcc 660

ctgttcgaga ggaatctacg acttctgctg atgcccctga gggcctgctg ctagatagga 720

cagctcgcct ggaggaagaa ccccccgag ttgcatacga agatgtatgc atgcgctctg 780

gttctgacac aacagcaaga gcagaatcct tagcagattc atcaagtcca ggacttttgt 840

gcttagatga gtccaaagca tttgcgaccc cggagccatt tgctcctcca ggaagcctgc 900

gccgagaagg atccattggt tcggtgggcc gctgcaggtc tcggcttcct gtagccccag 960

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aaatttgtga ctgctggtac ttcagaattg tccagtcaaa aacgtagtca aattgaaaac 1080

ctgtaaaact atttccagtt taggcaaaca gaagtggcac tgtaataaac tgaaaatcat 1140

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tttaaagaga acttccggct gcagaagttg aaaaggtctt cgagacttgg ccccaacaga 1860

tccagaacca agacattgta gtctccttct atcccgaacc atcctcgtgc 1910

<210> SEQ ID NO 7
<211> LENGTH: 720
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (58)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (613)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 7

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tgaaggtgtc aacgccgtga atagtgagcg ttgcgttatg aagattttga agccagtaaa 120

gaaaaaaaag atcaaaagag agatcaagat tctgcaaaac ctttgtggag ggcccaacat 180

tgtgaagctt ctggacattg tccgtgatca gcaatcgaag acacccagcc taatttttga 240

gtatgtgaac aatactgatt tcaaagtgct ctaccccact cttacagact ttgatatccg 300

atactacatt catgagctgc tcaaggcttt ggactattgc cattctcaag ggattatgca 360

cagggatgtg aagccacaca acgtgatgat tgaccatgag cagcggaagc ttaggcttat 420

tgactgggga cttgccgaat tctatcatcc tggcaaagag tataatgtgc gtgttgcctc 480

taggtacttc aagggtcctg agctgctggt tgatcttcaa gattatgatt actctctcga 540

catgtggagc tctggggtgc atgtttgccg gcatgatatt tcggaaggag ccattctttt 600

atgggcatga canttcatga tcaacttggt gaagatcgct aaggtgttgg gaacttgatg 660

aattgaattc ctatctaaca aataccgcta agtggacccc attggagcac ctggtggggg 720

<210> SEQ ID NO 8
<211> LENGTH: 953
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 8

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ggccttacaa cttgagatga agtgtgaagt ggtactgcac catatcatca ggacctaagc 180

tgcaatccag agcctccctc caaatgagat ccctgatagg ctcctccgag atagagggct 240

cctcgaagcc aaactcgaag ggagataccg agccaggctc atcgttgatg tcatgaagtg 300

aagcttaaat aagggtgcgc caaggcagct tccactgtga ttcttttcgc tggatcaaag 360

accagcatct tttcaacaag atcaagagca gaacgattaa tgcctctgaa cttctgggtt 420

aagggaatag gcgactgtcg aggcaggtgc ttgatatacc gcctagcatt gtcgcttctc 480

aaaaacccaa gatccctatc ttcaggagtt ccgatgagtt ctgtaattag gcggagctga 540

tgcacatagt ctctcccagg gaacaacgca gatcggttaa gcaactccat gaagatgcac 600

cccacagacc aaatgtcaat agctgcagtg tatgctgaac aattcaggag cagctctgga 660

gctctgtacc acctcgttac aacatactca gtcatgaaat ccgtttcaga gagagtgcgt 720

gccaagccaa aatctgcgat tttcaaatcg caattggcat tgacgagaag gttggtgggc 780

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ttcaagtccc ggtgcaagac gttcgccgaa tggatgtact tcaagccccg caagatttga 840

tacagaaaat actgacagtg gtcttctgtg agagcttgat ttgaacgaat gatctggtgt 900

aggtccgtat ccatcaactc gtatacaatg tacacgtcgt tgaaatctcg tgc 953

<210> SEQ ID NO 9
<211> LENGTH: 683
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (663)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (670)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 9

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taatctttcc ggagaggcct tatcgccgac ggcaactgcc gaagacgaga ttactcagat 180

gatactaaaa agtgccgcaa ggtccgaatt aggaatgtat gtttcgaaga gacaggaatt 240

ctatcttcga agagcgcgga ggcggcgtaa gtttgcgtgg aagccggttt tgcagagcat 300

ctccgagatg aagcctgtca tggaattcca cactccgatg gcttaccggg atagtgggtc 360

tccgccgaag aacgcctcta ccccatcctt acctggcccg aagaacattt caccgccacg 420

acaagtgagt gtcccgcaaa ggagcagtcc tccgccgaag aacgtctcac cacctcccca 480

gcccggcatt ttgtagcgcg gactgcgatc gaagtattct gctgcatctc agcaagttca 540

acgaaatcga gggcaacgcg aaatctcttt tatatggcgt agtttgtgtc tccgactgga 600

ctcctatcta tccccatcga gataactgat tcggtggata atttctccaa attttggcta 660

acncaagaan ctcaagggcg aat 683

<210> SEQ ID NO 10
<211> LENGTH: 1156
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (923)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1143)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 10

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aaaatctccg tgaggaaatt ccttgtcgca agacgtgaaa aaaagaagaa agaagatgga 180

aatattgttt tgggtatcga agaagtgttc gatgctgtgc aataaggaaa gaaaaagtgc 240

aggtaacata aaaagctagc atggtgatga taatataaga ccccgattaa cacacttatg 300

gattgtttca tgagctgcac gttctcagcg acaaatgggg ctcattgaga aaactccact 360

ttctataagg ttgggaaacg agcgtttttt ttttgaagat gtttttttccg tcaatctgat 420

ttgatatcgt tctcaacttg accacatatg actatataag gaaaaggcat tgagaaagtg 480

gcggattggc gaggtagttc gaccatgctt ttggtaaagt cccttgaagt tcagtggtgg 540

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atcaggcttg tggtagtgac agtctctgca cgccatgcga ggctaacttt aagttacaaa 600

atcttgctca aatggtactc ttcctcgttg tacttttgca ggaacggatg tttaagtaaa 660

tcagtagttg atggtcgttc actgggacat ttccggatgc aggattcaat aaaagaacaa 720

aattcggggg agaatttgtc aggggatgcg gctgcggggg gttgattaac tatacattcc 780

atgaggatga agaaattttg ccaaccctct tccattccag ctggtttgta tgggaaggta 840

cccaacgcac actccaaaag agtcaatcct aaactccata ggtcactgtc gtatgcatac 900

gaacgcccct gaaggcgttc tgncgacata tatgtgcaag tcccaacgaa cgtgtctcgc 960

tgggccaagg aatgaaccaa cacagcactg acaccaaaat cagatatttt gacctcaccc 1020

ttgtgattga tgaggaggtt ggagggcttt atatcacgat gtatgatgtg cctgacttgg 1080

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atntgctttc tggtgc 1156

<210> SEQ ID NO 11
<211> LENGTH: 629
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 11

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ggggaggtct tcgcgtcgcg gtgccgaagc aagagactcc cgtcagcaaa tttttgactg 180

ccagtggaac tttccaggat gatgatatca agctcaacca caccgggctt cgcgtcgtct 240

cttcagaacc taaccttcct acgcagacgc agtctagctc cccagatggg caactgtcaa 300

tagcagacct ggagttagtg cggttcttag gaaagggtgc gggtggaacc ggtgcagctt 360

ggtccggcac aaatggacca atgtcaatta tgcactgaag gcgatacaaa tgaatatcaa 420

cgaaacagtg aggaagcaga ttgttcagga gctgaaaatc aaccaagtga cgcaccagca 480

gtgcccttat atcgtggaat gcttccactc cttctaccac aacggcgtca tatccatgat 540

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tgagccgtat ttggccgtca ttgctagtc 629

<210> SEQ ID NO 12
<211> LENGTH: 514
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 12

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gatatgcgga aacgcatgac tgctgcacaa gctttaactc atccatggat tcgaagtaac 180

aacgtgaaga tacctctgga tatcttagtg tacagacttg tgaggaatta tcttcgtgca 240

tcatccatga gaaaggctgc tttgaaggcc ctgtcaaaga ctttaaccga agacgagact 300

ttttatctac gtactcaatt tatgctgcta gaaccaagta acaacggtcg tgttacttttt 360

gagaatttca gacaggcact gctgaaaaat tcaacagagg ccatgaaaga gtcacgggtt 420

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tgtgcagcgg ccattagtgt tctccagtta gaag 514

<210> SEQ ID NO 13

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<211> LENGTH: 1387
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1385)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 13

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aaatgtgaac gggctgcaag cttggttttg gagcaacgtt ggagcattga agggttgcgc 240

tcgtccctgc ccattcctcg cttctgctct ggcctatgtc atgacgacgt gaaggagagg 300

atttgagggt tttgcaagtg atataatcct ccccgaggag atttctgtga gttgattaac 360

ttggatcagc gacatgggga acactagttc gaggggatcg aggaagtcca ctcggcaggt 420

gaatcaggga gtcgggtctc aagacacccg agagaagaat gatagcgtca atccaaagac 480

gagacagggt ggtagcgttg gcgcaaacaa ctatggcgga aagcacaagc agtggtgctc 540

aggccggaga acgatccacc tctgcgcccg ctgctctgcc gaggccgaag ccagcatcga 600

ggtcagtatc cggtgttttg ggtaagccgc tgtcagatat tcgtcaatct tacatcctgg 660

gacgggagct tggccgaggg cagttcggag tgacttactt gtgtactgac aagatgacga 720

atgaggcgta cgcgtgcaag agcatcgcca aacggaaact gaccagtaag gaggatatcg 780

aggatgttaa gcgggaggtt cagattatgc atcacctgtc ggggacaccc aatatcgtgg 840

tgttaaagga tgtgttcgag gacaagcatt ccgtgcatct tgtgatggag ctctgtgcag 900

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ccacagactt cggtctgtca actttcttta agccaggaga tgtgttccag gatattgttg 1140

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aactgagcag ggtatctttg acgctgtgct caaagggcac atagacttcg agaacgagtc 1320

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tgaanat 1387

<210> SEQ ID NO 14
<211> LENGTH: 2784
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 14

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cggaaaggta ttttccgacg aagagtcaat gtgggcgtgg acaaacgttt gaagagatgg 180

gtgtggatat gaaggctccg gctaagcagt cgctgggagt cggactgctc ctgtgctctg 240

tagtgatcct ctcggtggtg agctctgtgt atggccaagt tcagacagat ccagtggata 300

ctacaggctt aatttccatg tggtatgact taaaacagag tcaatctctc acggggtgga 360

ctcaaaatgc ttctaaccct tgtgggcagc agtggtacgg cgttgtatgt gatggctctt 420

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ttcaaaacgc ttttaaaaag cttcgaattt ttgatgctag taacaacaac atcgaaggaa 540

atattcctca acagtttcct acgtctctta ctcaaatgat attgaacaac aataaattga 600

ccggaggtct cccacagttt gatcaattgg gcgccttgac agtcgtaaac ttgagcaaca 660

acaatctgac cggcaacatg aaccccaact atttcaatgt gatcgtgaat gtggaaacct 720

tcgatgtttc ctataaccaa cttgaaggca ctcttcccga ctccattcta aacctggcca 780

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gtaagagtga gaagaaaagt tcaaagcaca gagtatttga gccagctcct cttgacaaag 1320

gagcagccga cgaaccagtg gtgaaggcgt ctccgcccgt caaggtactg aaggctcctc 1380

cttcatttaa gggtatcagc ggcctgggtg ctggacattc gaaagcaaca attggcaagg 1440

tgaacaagag caatattgca gccaccccat tctctgtagc ggatcttcag gcagccacaa 1500

acagcttctc ccaggataat ctgattggag aagggagcat gggtcgcgtg tatcgtgccg 1560

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agaatgagga tgacttcttg agtgtagtag acagtttggc tcgcctgcag catgctaata 1680

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tgagtcgtgg aaccctgaac gaattgctcc atttctcggg tgaaaacacc aaggccctgt 1800

cctggaatgt ccgcattaag attgctttgg gatccgcgcg tgctctggag tacttgcacg 1860

aagtctgtgc acctcccgtg gttcaccaca acttcaaatc tgccaatatt ctgctagacg 1920

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gatgggccac acctcaattg cacgacatcg acgcccttgc acgaatggtg gatccgtcgt 2220

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acgagccatc tgagacttca ctttgagagt actgaagcgc ccactagcct aatcgtgcat 2460

ctttggccat ctcgtttctg agtggaacac aagctgggta tattctttgg tggttaagca 2520

acattttgtc acaatttgaa cttcagctgg agaagggtct gtagtgttga agaaaacgaa 2580

tgcaaagcgt ttcggcgtgg atgtgctttg agaacttaca aaactcatca agactttgaa 2640

gatctttgta ttgcatcgaa tcctttcaat cagtctcggg taggatcagt tcctctgtat 2700

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tagtgacctt ggtcgagtta acgc 2784

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<210> SEQ ID NO 15
<211> LENGTH: 1088
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 15

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gctgtgtgag tgagtgagtg agtgagtgcg tgagtgagga tgtctgtttc tggtatggac 120

aactatgaga agctggagaa ggtaggagag gggacttacg gaaaggtgta taaggcccgt 180

gataaacgct ccgggcagct ggtggcgctc aagaagacta ggttggagat ggaggaagaa 240

ggcgtccctt ccaccgcttt gcgcgaagtt tcgttgctac aaatgctctc ccacagcatg 300

tatatcgtca ggctactttg cgtggagcac gtcgagaaag gcagcaagcc catgctctac 360

ttggtctttg aatatatgga cactgatctt aagaagtata ttgacttgca cggtcgtggt 420

ccgagcggga agcctctgcc tcccaaagtg gtccagagtt tcatgtatca attgtgcaca 480

gggcttgccc actgtcatgg ccacggagta atgcacaggg atctgaaacc ccagaatttg 540

ctcgtcgaca agcaaacccg tcgtcttaag attgccgacc ttggtctcgg tcgggcattc 600

acagtgccaa tgaagagtta cacacacgag attgttactc tatggtaccg agctcctgaa 660

gttcttcttg gagcgaccca ctactctcta cctgtggata tctggtctgt tgggtgcatc 720

ttcgctgaac tcgtccggaa aatgccgctc ttcactggag actccgaact tcagcagctt 780

cttcacatct tcaggttgct tggcaccccg aatgagacaa tctggcctgg tgttagccag 840

caccgtgatt ggcacgagtt tcctcaatgg agaccacaag atctgtccct tgctgttccc 900

ggactcagcg cggttggctt agaccttctc gccaaaatgt tggtattcga gccctcaaag 960

agaatctctg ccaaagccgc cttgagccat acttatttcg ctgatgttga taagacagca 1020

acctaaacac aacagaacaa ttcaagagaa ccaggtaacc tctacctgtc caagacgaag 1080

gttaacgc 1088

<210> SEQ ID NO 16
<211> LENGTH: 1627
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 16

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cggaaatgca ctgggctgtg aggagtaacg acgtggggct gttaaggacc attctgaaga 120

aagacaagca gctcgtgaat gctgcggact atgacaagcg cacgcccttg cacatcgccg 180

cgtccctgga ttgtgtccct gttgctaaag tcctgcttgc ggaaggagca gagttgaatg 240

caaaagacag gtgggggaaa tctccgagag gcgaggcgga gagtgcagga tacatggaga 300

tggtaaagct gttgaaggat tacggggctg agtcacacgc aggtgccccg aggggccacg 360

ttgagagtct gattcaggtt gcccctccgt tgccttctaa ccgcgactgg gagatcgctc 420

cgtcggagat tgaacttgat accagcgagc tcatcggcaa aggcgccttt ggagagattc 480

ggaaggcgct ttggcgcggc acacccgtcg ctgtgaagac aatcagacct tctctgtcca 540

acgacagaat ggtcatcaag gacttccagc acgaggtgca attgctcgta aaggttcggc 600

acccaaacat tgtgcagttc ctcggggctg ttacccgtca aagacctctc atgttagtca 660

ccgagtttct ggcaggggggc gatttgcatc agttgctgag gagcaaccct aatttggctc 720

ctgaccgcat cgtgaagtat gccctcgaca tagctcgcgg catgtcttac cttcacaatc 780

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ggagcaagcc catcatccac cgcgatctca aaccccgaaa catcatagtg gacgaagagc 840

atgagctgaa ggtcggcgac ttcggactga gcaagctgat cgacgtaaag cttatgcatg 900

atgtgtacaa gatgacgggg gggactggga gttacagata catggcgcct gaggtcttcg 960

aacatcaacc ctacgacaaa tccgtcgacg tgttttcctt tggaatgata ttatatgaga 1020

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tgcaatttct tctccgacga ccacattgcg acatgaagca ccagactttg gatgtagaag 1500

gcatggtcta catgctttgc tgtgagcctt gcacgtctcg caggttgatc tctttaacca 1560

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ttaacgc 1627

<210> SEQ ID NO 17
<211> LENGTH: 1441
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 17

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agaactcttt tcaagcaact gaggccttcc ccattcgtgc cgcatctctt ggccacccct 180

attgacagtg acaatgtggc actcgttctt aattgtgtgt tagctgggcc tctagaactt 240

ctacttcggt caccttaga cgagaactca gctcgttttc tggtcgccaa cgtggtatta 300

gccgtcgaac ttctgcacaa ggatggcgtt gtatatcgtg gcatctctcc cgatgttctt 360

atgatagatc ggaaaggacg acttcagctg gttgattttc ggtttgcaaa gcaaatgtcg 420

gatgagcgca ctttcacagt ctgtggcatg gctgatttct tagcacccga gatcattcaa 480

ggacaaggtc atggcctggc ttctgactgg tgggcggtag gtgtgttaat gtacttcatg 540

ttgcaaactg agcttccatt tggatcatgg cgggacaacg agcttgaaat ttttggtaga 600

atagcccgtc ggcagcttac gtttccttca agtttcagcc ctgaagcggt tgacctcatt 660

gacaagctgc tggtggtgga cccaaccaag agactgggct gtgacagcca tggatcgctt 720

gccataaggg aacatccttg gttccgaggt ataaactggg acaagcacct cgattgcagt 780

gtggaagttc cttcagagat catgacacgc cttcagttgg ccatagactt tcttcccgtg 840

gatgatagtt atcaagtgtt tgatctccaa cccgatgaag acgatccacc atggcttgat 900

ggctggtgat agcttgatgg ctcgtagatc ccccttctcc aagcatcaat ggcacagtac 960

cgaatggcta taacagaaga tgcacattaa gtgctccatg aacagatacc gtagcgctta 1020

ggatttttcg gtcgtcacaa atgacggctc tcttgtgagg ttcgaatgtt gtgtcacccg 1080

atgatctcta ctggcacaaa cctccaggct gaatcttaag gccagctgtt ttaggtgaga 1140

cgtttacctt ggttcgaact cacgctcgtg ttgttaagcg cgagtcgatg atgtatgaaa 1200

tgacggtgtt ccttgaaagt cttgaaaggc aatcaattcg cttatgtgtg tcccttccat 1260

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gtggtcatta gggaagggaa ccgctgcact agtcagtaaa cgaacatggc ttcaattgta 1320

tagcatagcg gtagaggttt cgtacgaaat gtggttgcag tcggtgatta taggcgcatt 1380

tctctgaaca tgcacgagaa tcgtgctcct gagtctccat cattcagtgg tgcgagctcg 1440

c 1441

<210> SEQ ID NO 18
<211> LENGTH: 1736
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 18

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tgggaggtga tcgcatgaga gctcctcaga ggcagtctcg agaatatcaa tatagatcat 180

tggacgtctt cacagagcag cacgagcagt tgcaaaagca gcagcagcaa gatgagtatc 240

agagaacaga attgaagctc gagacactgc caaaaatgtt aagcaatgcg accgtgtcat 300

cttcccctcg aagcagtccg gatggacgta gactacgtac agtcgcgaat aagtatgctg 360

tggaaggtat ggttgggagt ggcgcattct gcaaggtgta tcagggctcc gatttgacga 420

accacgaggt tgtgggcatc aagctggagg atacgagaac tgagcacgct cagttaatgc 480

acgagtcgcg cttgtacaac atattgcggg gtgggaaggg agtgcccaac atgagatggt 540

tcggaaaaga gcaagactac aatgtgatgg tgctagacct attggggccg aacctgttgc 600

acctctttaa ggtgtgtggg ctaaggtttt cgttgaagac cgtgattatg ctcggttacc 660

aaatgattga ccgggtggaa tacgtgcatt ctcgagggct cgttcaccgt gacctgaagc 720

cggataactt cctcatgggc tgcggtcggc aaggaaacca agtgttcatt atagattttg 780

gcttggcaaa ggagtacatg gacccggcaa cacgaaggca tatcccttac cgagatagga 840

agagcttcac agggacggca cggtacgcta gtaggaatca gcacagagga atcgagcaca 900

gtagaagaga tgacatagaa tcacttggtt acattcttat gtactttcta agaggcaatt 960

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acaacaaaat caagatgaac accactgtgg aggagctttg tgatgggtat cccagtcaat 1080

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atttttactc ggaaagccca tgacggtgat gatttcaata cgttgcacaa gcaactttct 1680

tctgtaattg aaatagagga tctggtctga gtatgagaag atgggcatgt taacgc 1736

<210> SEQ ID NO 19
<211> LENGTH: 1900
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

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<400> SEQUENCE: 19

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taggggaggc atgcgggagc aggattggtg ttaagttcgt aaggagaagg gagtacatgc 120

aagtgcgtgc ttgtcggata tcggacagct ggatttgtaa ataagcggag aggagggtcg 180

gtaatcaggg gcgtacatcg atggagccgc gtgtgggaaa caagtatcgg ctgggacgga 240

aaattgggag cggttccttt ggggagatct atcttgggac caatgttcag accaatgagg 300

aggtcggaat aaagctggaa agcatcaaga cgaagcatcc acaattgctg tacgagtcca 360

agctctaccg gatactacaa ggaggaactg ggattcccaa tatcagatgg ttcgggatag 420

aaggagacta caatgtcttg gttctggatc tgttggggcc aagtctcgaa gacctttca 480

acttctgcag ccggaagttc tctttaaaga ctgttctcat gcttgctgac cagctgatca 540

acagagtgga gtatgtgcat gcgaaaagct ttcttcatag agacatcaag cctgataatt 600

ttctaatggg gcttggtagg cgagcaaacc aggtctacat tattgatttt ggtcttgcca 660

agaagtaccg cgacccttcc acgcatcagc atattcccta cagggagaac aaaaatctga 720

cagggactgc tcggtatgca agcatcaaca ctcatcttgg tattgagcaa agcagacgag 780

atgatttgga atctcttgga tatgtgctca tgtacttcct gagaggcagt cttccatggc 840

aaggactgaa agcgggaacc aagaagcaga agtacgagaa gatcagtgag aaaaaaatgt 900

ccacgcccat tgaggtcctt tgtaaaaatt atccttcaga attcgcctcg tacttccact 960

actgccggtc cttgcgtttt gatgacaaac ccgactatgc atatttgaaa agaatcttcc 1020

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aaccaatgga tccttctcgg cgcaggcttc ctggaggagc aaatggctcc ggggtcgcaa 1260

atgctttgga ctcatctaag cacaaaagtc ctggacttga tgaatctgct aaggattctg 1320

ctcttgctgt tgtgtcagaa ccagagcgca tgcatacatc ttcgtatgca actcgggggg 1380

gttcttcctc caggcgagct gtcctatcta gcagcaggcc ctcaggggca tcagcagaag 1440

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cagggatgca gaggagctct ccagttactt cggacccaaa gcggatatct agccgccatc 1560

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gtgtggtagc tctctgccat acgattccta aggttaacgc 1900

<210> SEQ ID NO 20
<211> LENGTH: 1217
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 20

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ggtgttatgt ccaaggcccg ggtttacaca gatgtgaatg tccaacgtcc gaaagattat 180

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aaggtggggc gagggaaata cagtgaggtt tttgaaggtg tcaacgccgt gaatagtgag 300

cgttgcgtta tgaagatttt gaagccagta aagaaaaaaa agatcaaaag agagatcaag 360

attctgcaaa acctttgtgg agggcccaac attgtgaagc ttctggacat tgtccgtgat 420

cagcaatcga agacacccag cctaattttt gagtatgtga acaatactga tttcaaagtg 480

ctctacccca ctcttacaga ctttgatatc cgatactaca ttcatgagct gctcaaggct 540

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attgaccatg agcagcggaa gcttaggctt attgactggg gacttgccga attctatcat 660

cctggcaaag agtataatgt gcgtgttgcc tctaggtact tcaagggtcc tgagctgctg 720

gttgatcttc aagattatga ttactctctc gacatgtgga gcttggggtg catgtttgcc 780

ggcatgatat ttcggaagga gccattcttt tatgggcatg acaattatga tcaacttgtg 840

aagattgcta aggtgttggg aactgatgaa ttgaattcct atctaaacaa ataccgccta 900

gagctggacc cccatttgga agcactggtt ggcaggcata gcaggaaacc ttggtcaaag 960

ttcatcaatg ctgataatca gcgtctggtt gttccagagg ctgtggattt tttggataag 1020

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ttttatcccg tgaaggtgtc ggaggttagc aaccgtcgca gtgcttgata tgaattgata 1140

tatctcatat gggctttctt gtgattacgt cccacccggc taccaggttt ctcagttgtg 1200

cgaagcgctg agctcgc 1217

<210> SEQ ID NO 21
<211> LENGTH: 1718
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 21

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tcgcccccgc ctcgcccttc accctcctct gttcttgtca cagcctcctc ctccgtctct 120

gtctgttggc tgggtaagtt ttgggagtga ggaggacgtg gtcatggaag aagagccccc 180

ctcttttgta gtggactgtc ggtaaattgg acctggagcc tgccggctca tcgcgtttgc 240

ttagattgtg ggcgggtgct gttgaaattc cttgaacttg ctactggtcg gaaacgctcg 300

aattgcgact ttgattgaag gtctggttgt tgctgcggtc gggatcttac tcagtctctt 360

caataggacc tctgaagcag tatggagact agcagtggaa ctccagaatt gaaagttata 420

agtactccga cctacggagg tcattacgtg aaatatgttg tggcgggaac tgatttcgaa 480

gtcaccgcga ggtacaagcc accacttcgt ccgattgggc gcggagctta tggaatcgtc 540

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ttcgacaaca ggatcgatgc gaagcgaaca ctgcgtgaaa taaaactcct ccggcatatg 660

gatcatgaaa acgtcgttgc cattacagac atcattcgtc ccccaactag ggagaatttc 720

aacgacgtgt acattgtata cgagttgatg gatacggacc tacaccagat cattcgttca 780

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aagtacatcc attcggcgaa cgtcttgcac cgggacttga agcccaccaa ccttctcgtc 900

aatgccaatt gcgatttgaa aatcgcagat tttggcttgg cacgcactct ctctgaaacg 960

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tgttcagcat acactgcagc tattgacatt tggtctgtgg ggtgcatctt catggagttg 1080

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attaatcgtt ctgctcttga tcttgttgaa aagatgctgg tctttgatcc agcgaaaaga 1320

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catatcaagg atctcatttg gagggaggct ctggattgca gcttaggtcc tgatgatatg 1500

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catttcatcc agcagacatt gttgctcggc gttaacgc 1718

<210> SEQ ID NO 22
<211> LENGTH: 2177
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 22

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aggtctctga gctgagaatg tttgcaattt aggggcacca ccggtttgtt ggagtccctt 240

gccacttatt acaattgttg gtttacaagc tcgacgagtt tcaatcgaac gtagagtttt 300

agtcgggtcg aggatctatg tatccgctca gcggagaaga gagcctgatg ttgccgaagc 360

gatcgtgtgg gatttgacta gaaagaggtg gaccgcatca gaactattta ttccttgtga 420

gggaaggatc gaggttccaa tgggtctcac tccgttttct tgtgtcacgg ttcaaggtta 480

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catacgaaac gagggcccag agcctcacct cgctggagac cgaccatcga agcaccttaa 900

gctcgttttc attcggcatt gcttgcgagc acttcgactt cctagaattt caatagacct 960

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ttaccgggat agtgggtctc cgccgaagaa cgcctctacc ccatccttac ctggcccgaa 1260

gaacatttca ccgccacgac aagtgagtgt cccgcaaagg agcagtcctc cgccgaagaa 1320

cgtctcacca cctccccagc ccgcatttgt agcgcggact gcgtcgaagt attctgctgc 1380

atctcagcaa gttcaacgaa atcgaggcaa cgcgaaatct ctttatatgg cgtagtttgt 1440

gtctcgactg aactcctatc tattccccca tcgagataac tgcattcgtt ggataaattt 1500

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ctccaacatt tttgctcttc atcctcaagc agctcctcaa tggccagtaa tatgttacga 1560

cattgtgcac aactccaatt acgtagcgtt attctgtaac ccacgttcat cgaggtatca 1620

aggaatggcg cagtaagcac tgctactttg tgctttggta tcccgttgtg acgagatgtc 1680

atgtcgcacc gtgcctatca gtgggatttt cttgagcgca gatcttgctt ccgcagtttg 1740

tttcataacg ttttggttcg taggggggcct agacggtact atcaagcaat gagaagtgtg 1800

ctggtgtgga tttgacagca atcttttgga ggattgtctt tcctatgtag aacatagcga 1860

ggacacttgc gcctggtggg cacatcccat agaacatagt gcttcacttc tgggttgttc 1920

accactagga tcatatgacc ttctcatcta ttttcgggct ttgtttcgag ctcatgtacc 1980

atcgactagc gtcactttga ctgcggtgat aatcgtttgt caatttagtg gagctttgta 2040

gatgatagat gccatttgta cagtagcttg gatgctgttt acaagatagc ggcagctaga 2100

agccttaaac ctttagctac catgtattat ttaaacctat atgaagtgaa cggctgtgca 2160

gatattgccg ttaacgc 2177

<210> SEQ ID NO 23
<211> LENGTH: 1731
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 23

atcccgggcg gtcgagtcgt attaggtgtt gtttcattgt aagggttcgg aagcacgggg 60

cacggcgtat ataccgttcc ccttgaacgt tgatctcacc tttggaagac ctgaattgag 120

tagcgtgcgg aagctgcatc gatccggaag agacgatgag taggagagtg agaaggggag 180

gtcttcgcgt cgcggtgccg aagcaagaga ctcccgtcag caaatttttg actgccagtg 240

gaactttcca ggatgatgat atcaagctca accacaccgg gcttcgcgtc gtctcttcag 300

aacctaacct tcctacgcag acgcagtcta gctccccaga tgggcaactg tcaatagcag 360

acctggagtt agtgcggttc ttgggaaagg gtgcgggtgg aaccgtgcag cttgtccggc 420

acaaatggac caatgtcaat tatgcactga aggcgataca aatgaatatc aacgaaacag 480

tgaggaagca gattgttcag gagctgaaaa tcaaccaagt gacgcaccag cagtgccctt 540

atatcgtgga atgcttccac tccttctacc acaacggcgt catatccatg atcctagagt 600

acatggacag gggctcgttg tccgacatta ttaagcaaca aaagcagata cctgagccgt 660

atttggccgt cattgctagt caagttctga agggattgga atacctacac caagtcaggc 720

acatcataca tcgtgatata aagccctcca acctcctcat caatcacaag ggtgaggtca 780

aaatatctga ttttggtgtc agtgctgtgt tggttcattc cttggcccag cgagacacgt 840

tcgttgggac ttgcacatat atgtcgccag aacgccttca ggggcgttcg tatgcatacg 900

acagtgacct atggagttta ggattgactc ttttggagtg tgcgttgggt accttcccat 960

acaaaccagc tggaatggaa gagggttggc aaaatttctt catcctcatg gaatgtatag 1020

ttaatcaacc ccccgcagcc gcatcccctg acaaattctc ccccgaattt tgttctttta 1080

ttgaatcctg catccggaaa tgtcccagtg aacgaccatc aactactgat ttacttaaac 1140

atccgttcct gcaaaagtac aacgaggaag agtaccattt gagcaagatt ttgtaactta 1200

aagttagcct cgcatggcgt gcagagactg tcactaccac aagcctgatc caccactgaa 1260

cttcaaggga ctttaccaaa agcatggtcg aactacctcg ccaatccgcc actttctcaa 1320

tgccttttcc ttatatagtc atatgtggtc aagttgagaa cgatatcaaa tcagattgac 1380

ggaaaaaaca tcttcaacgc cgtttcccaa ccttatagaa agtggagttt tctcaatgag 1440

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ccccatttgt cgctgagaac gtgcagctca tgaaacaatc cataagtgtg ttaatcgggg 1500

tcttatatta tcatcaccat gctagctttt tatgttacct gcacttttc tttccttatt 1560

gcacagcatc gaacacttct tcgataccca aaacaatatt tccatcttct ttcttctttt 1620

tttcacgtct tgcgacaagg aatttcctca cggagatttt tcaacacttt tctcaaatgt 1680

ttttagagtt tttaaactga caattgaaga ggtcggacct accggactcg c 1731

<210> SEQ ID NO 24
<211> LENGTH: 1407
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 24

atcccgggag aggctgatct gatgctacag tttcgtgtgc agctagtctt tagagattcg 60

ggcaacgcac ttgttgaaga tcggaaactt tcaaaatcgg tcgagtcgta ttaggtgttg 120

tttcattgta agggttcgga agcacggggc acggcgtata taccgttccc cttgaacgtt 180

gatctcacct ttggaagacc tgaattgagt agcgtgcgga agctgcatcg atccggaaga 240

gacgatgagt aggagagtga gaaggggagg tcttcgcgtc gcggtgccga agcaagagac 300

tcccgtcagc aaatttttga ctgccagtgg aactttccag gatgatgata tcaagctcaa 360

ccacaccggg cttcgcgtcg tctcttcaga acctaacctt cctacgcaga cgcagtctag 420

ctccccagat gggcaactgt caatagcaga cctggagtta gtgcggttct taggaaaggg 480

tgcgggtgga accgtgcagc ttgtccggca caaatggacc aatgtcaatt atgcactgaa 540

ggcgatacaa atgaatatca acgaaacagt gaggaagcag attgttcagg agctgaaaat 600

caaccaagtg acgcaccagc agtgccctta tatcgtggaa tgcttccact ccttctacca 660

caacggcgtc atatccatga tcctagagta catggacagg ggctcgttgt ccgacattat 720

taagcaacaa aagcagatac ctgagccgta tctggccgtc attgctagtc aagttctgaa 780

gggattggaa tacctacacc aagtcaggca catcatacat cgtgatataa agccctccaa 840

cctcctcatc aatcacaagg gtgaggtcaa aatatctgat tttggtgtca gtgctgtgtt 900

ggttcattcc ttggcccagc gagacacgtt cgttgggact tgcacatata tgtcgccaga 960

acgccttcag gggcgttcgt atgcatacga cagtgaccta tggagtttag gattgactct 1020

tttggagtgt gcgttgggta ccttcccata caaaccagct ggaatggaag agggttggca 1080

aaatttcttc atcctcatgg aatgtatagt taatcaaccc cccgcagccg catcccctga 1140

caaattctcc cccgaatttt gttcttttat tgaatcctgc atccggaaat gtcccagtga 1200

acgaccatca actactgatt tacttaaaca tccgttcctg caaaagtaca acgaggaaga 1260

gtaccatttg agcaagattt tgtaacttaa agttagcctc gcatggcgtg cagagactgt 1320

cactaccaca agcctgatcc accactgaac ttcaagggac tttaccaaaa gcatggtcga 1380

actacctcgc caatccgcca gagctca 1407

<210> SEQ ID NO 25
<211> LENGTH: 2253
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 25

atcccgggtg taggcgggcg aggttcgatg caatggggca gtgttatgga aagtttgatg 60

atggaggcga aggggaggat ttgtttgagc ggcagaaagt gcaggtttct aggacgccaa 120

agcatggatc gtggagcaat agcaaccgag ggagcttcaa caatggcggg ggggcctcgc 180

-continued

ctatgagagc caagacgtcg ttcgggagca gccatccgtc cccgcggcat ccctcagcta 240

gtccgctccc tcactacacg agctccccag cgccttcgac cccgcgacgg aacattttca 300

aaaggccttt tcctcctcct tctcccgcga agcacattca gtccagtctc gtgaaacggc 360

atggcgcgaa gccgaaagaa ggaggggcga tccctgaggc tgtcgatggt gagaagccct 420

tggataagca tttcggctat cacaagaact tcgctactaa gtatgagctg gggcatgaag 480

tcggtcgcgg gcacttcggt cacacatgtt acgcgaaagt acggaagggc gagcataagg 540

gacaagccgt ggcagtgaag ataatctcga aagcgaagat gacgactgct attgcgatcg 600

aggacgtggg acgagaagtg aaaattttga aggctctgac gggacaccag aatttggttc 660

gattctacga ttcctgcgag gaccatctaa atgtgtacat tgttatggaa ttatgtgaag 720

gaggtgaatt attggatcga attttgtctc ggggagggaa gtactcggag gaagacgcca 780

aggttgttgt gcggcagatt ttgagcgttg ttgcgttttg tcacctgcaa ggcgttgttc 840

accgagatct taagcctgag aattttctgt ttaccacgaa ggatgaatat gctcagctta 900

aggccattga ttttggattg tcagatttca tcaaacccga tgaaagactg aacgatatcg 960

ttggaagcgc atactacgtt gcgccggagg tattgcatag gttatattca atggaagctg 1020

acgtatggag cattggagtc atcacgtaca ttttgttatg tggtagtcga ccgttttggg 1080

cgcggaccga gtcgggcatt tttcgtgcgg tgttgagggc tgacccgagc tttgaagaag 1140

ccccttggcc ttccatctct cccgaagcca aggatttcgt gaagcgtctc ctgaataagg 1200

atatgcggaa acgcatgact gctgcacaag ctttaactca tccatggatt cgaagtaaca 1260

acgtgaagat acctctggat atcttagtgt acagacttgt gaggaattat cttcgtgcat 1320

catccatgag aaaggctgct ttgaaggccc tgtcaaagac tttaaccgaa gacgagactt 1380

tttatctacg tactcaattt atgctgctag aaccaagtaa caacggtcgt gttacttttg 1440

agaatttcag acaggcactg ctgaaaaatt caacagaggc catgaaagag tcacgggttt 1500

ttgaaattct ggaatcgatg gatggtcttc atttcaagaa aatggacttt tcagagttct 1560

gtgcagcggc cattagtgtt ctccagttag aagccacaga acgatgggag cagcatgctc 1620

gcgcagctta cgacatattt gagaaagagg gtaaccgagt catttatcct gatgaacttg 1680

cgaaagagat gggactagca ccaaatgtac cagcccaagt gtttctagat tggattagac 1740

agtctgatgg tcggctgagt ttcactgggt tcaccaagct gctacatgga atttccagcc 1800

gtgctatcaa aaatctccag cagtgattct ttgcatcgta cagttcggaa tggagttttt 1860

aagctctttt agtttcactt ccgtcttcaa ctgctgcttc gcctcgtctc tgagctgtga 1920

tagcgtatct caagcatatg cacaactcgc atttttgctg aagtgatttg tcacctcaca 1980

ttagtcgggc ctctggaact ttcacttatt tggattattt atgtagaagt ccagatcaaa 2040

aagcgaaaag gaatggctag atattgtcac aagaagtaac atagtcaaat tcaggagcac 2100

ttaagcacac attgagtgct ttttattgga attcttagat atggaactga tgtttccaag 2160

ggaagggtct atgaggcaga gagtggaatg tatagactgg catatggtta agtgatcatt 2220

ggactgccgt tctactccgg ttgtcgttaa cgc 2253

<210> SEQ ID NO 26
<211> LENGTH: 2230
<212> TYPE: DNA
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 26

atcccgggcg aactgcgatc tgagattcca acttggaagg gcctcgcgta agaccggatc 60

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tcgtttctta cgcttttgcg cctcgcgata tttgtacatt gtttcctctg gttttattcg    120

attccgcctc tgaaaatgtg aacgggctgc aagcttggtt ttggagcaac gttggagcat    180

tgaagggttg cgctcgtccc tgcccattcc tcgcttctgc tctggcctat gtcatgacga    240

cgtgaaggag aggatttgag ggttttgtaa gtgatataat cctccccgag gagatttctg    300

tgagttgatt aacttggatc agcgacatgg ggaacactag ttcgagggga tcgaggaagt    360

ccactcggca ggtgaatcag ggagtcgggt ctcaagacac ccgagagaag aatgatagcg    420

tcaatccaaa gacgagacag ggtggtagcg ttggcgcaaa caactatggc ggaaagccaa    480

gcagtggtgc tcaggccgga gaacgatcca cctctgcgcc cgctgctctg ccgaggccga    540

agccagcatc gaggtcagta tccggtgttt tgggtaagcc gctgtcagat attcgtcaat    600

cttacatcct gggacgggag cttggccgag ggcagttcgg agtgacttac ttgtgtactg    660

acaagatgac gaatgaggcg tacgcgtgca agagcatcgc caaacggaaa ctgaccagta    720

aggaggatat cgaggatgtt aagcgggagg ttcagattat gcatcacctg tcggggacac    780

ccaatatcgt ggtgttaaag gatgtgttcg aggacaagca ttccgtgcat cttgtgatgg    840

agctctgtgc aggtggcgag ctcttcgatc gcatcattgc caaggggcat tacagtgagc    900

gcgccgctgc cgatatgtgc agagtcatcg tcaatgtggt gcacagatgc cactcattag    960

gggtcttcca tcgggatctc aagccagaga attttctgtt ggccagcaag gctgaggatg   1020

cgcctctgaa ggccacagac ttcggtctgt caactttctt taagccagga gatgtgttcc   1080

aggatattgt tggaagtgcg tattacgtgg cccctgaagt tttgaagaga agttatggtc   1140

ctgaagctga tgtttggagt gcaggcgtga ttgtgtacat tctgctgtgt ggtgtacccc   1200

ccttctgggc tgaaactgag cagggtatct ttgacgctgt gctcaaaggg cacatagact   1260

tcgagaacga tccatggccg aaaatctcca acggggctaa ggatttggtg aggaaaatgc   1320

taaaccctaa cgtgaagata cgtctgacgg cacagcaggt gttgaaccat ccatggatga   1380

aggaagatgg tgatgctcca gacgtgccac tcgacaatgc ggtgttgacc agactgaaaa   1440

atttctcagc cgccaacaag atgaaaaagc tggcgctgaa ggtgattgca gagagtctgt   1500

cggaggaaga gatcgtgggg ttgagggaga tgttcaaatc catagataca gacaacagcg   1560

gcacggtgac gttcgaggag cttaaggaag ggttgctgaa gcagggctca aaacttaatg   1620

aatcggacat caggaaacta atggaagctg cagatgtcga tggaaacggc aagatcgact   1680

tcaacgagtt catatcggca acaatgcaca tgaacaagac ggagaaagag gatcaccttt   1740

gggcagcatt catgcatttc gacacggaca atagcgggta tatcaccatc gacgagcttc   1800

aggaagcaat ggagaagaat ggaatgggag atcctgagac catccaagag atcatcagcg   1860

aggtggacac agacaacgac ggaagaatag actacgacga gttcgtagcc atgatgcgca   1920

agggcaatcc tggcgctgaa aacggaggaa cggtgaacaa gcccagacac aggtagtagc   1980

tcctggttgc caatttgacg acgggtttgg caaggcaaca gtagttgttg ttagctttca   2040

gattcaggtt cggtattgtt catgccctcc tttgtctcga acaatggact ctaggccttt   2100

ccaatggaaa agctattcca acagggtttg cataacgtgt agtagaatga aagcattgcc   2160

tgggggggtgt acagtgcctg tgatcttgtg gagttctcgt aggatggctt cggttggatc   2220

tcgttaacgc                                                          2230
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<210> SEQ ID NO 27
<211> LENGTH: 749
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

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<400> SEQUENCE: 27

```
Met Gly Val Asp Met Lys Ala Pro Ala Lys Gln Ser Leu Gly Val Gly
 1               5                  10                  15

Leu Leu Leu Cys Ser Val Val Ile Leu Ser Val Val Ser Ser Val Tyr
            20                  25                  30

Gly Gln Val Gln Thr Asp Pro Val Asp Thr Thr Gly Leu Ile Ser Met
        35                  40                  45

Trp Tyr Asp Leu Lys Gln Ser Gln Ser Leu Thr Gly Trp Thr Gln Asn
    50                  55                  60

Ala Ser Asn Pro Cys Gly Gln Gln Trp Tyr Gly Val Val Cys Asp Gly
65                  70                  75                  80

Ser Ser Val Thr Glu Ile Lys Ile Gly Ser Arg Gly Leu Asn Gly Asn
                85                  90                  95

Phe Asn Pro Ser Tyr Phe Gln Asn Ala Phe Lys Lys Leu Arg Ile Phe
            100                 105                 110

Asp Ala Ser Asn Asn Asn Ile Glu Gly Asn Ile Pro Gln Gln Phe Pro
        115                 120                 125

Thr Ser Leu Thr Gln Met Ile Leu Asn Asn Asn Lys Leu Thr Gly Gly
    130                 135                 140

Leu Pro Gln Phe Asp Gln Leu Gly Ala Leu Thr Val Val Asn Leu Ser
145                 150                 155                 160

Asn Asn Asn Leu Thr Gly Asn Met Asn Pro Asn Tyr Phe Asn Val Ile
                165                 170                 175

Val Asn Val Glu Thr Phe Asp Val Ser Tyr Asn Gln Leu Glu Gly Thr
            180                 185                 190

Leu Pro Asp Ser Ile Leu Asn Leu Ala Lys Leu Arg Phe Leu Asn Leu
        195                 200                 205

Gln Asn Asn Lys Phe Asn Gly Lys Leu Pro Asp Asp Phe Ser Arg Leu
    210                 215                 220

Lys Asn Leu Gln Thr Phe Asn Ile Glu Asn Asp Gln Phe Thr Gly Asn
225                 230                 235                 240

Tyr Pro Ser Gly Leu Pro Ser Asn Ser Arg Val Gly Gly Asn Arg Leu
                245                 250                 255

Thr Phe Pro Pro Pro Pro Ala Pro Gly Thr Pro Ala Pro Arg Thr Pro
            260                 265                 270

Ser Pro Ser Gly Thr Ser Asn Gly Ser Ser Ser His Leu Pro Leu Gly
        275                 280                 285

Ala Ile Ile Gly Ile Ala Ala Gly Gly Ala Val Leu Leu Leu Leu Leu
    290                 295                 300

Ala Leu Gly Ile Cys Leu Cys Cys Arg Lys Arg Ser Lys Lys Ala Leu
305                 310                 315                 320

Gly Asp Pro Glu Ala Thr Thr Ser Ser Arg Arg Pro Trp Phe Thr Pro
                325                 330                 335

Pro Leu Ser Ala Lys Ser Gln Ser Asp Pro Ser Lys Ser Ile Asp Lys
            340                 345                 350

Thr Thr Lys Arg Asn Ile Phe Gly Ser Ser Lys Ser Glu Lys Lys Ser
        355                 360                 365

Ser Lys His Arg Val Phe Glu Pro Ala Pro Leu Asp Lys Gly Ala Ala
    370                 375                 380

Asp Glu Pro Val Val Lys Ala Ser Pro Pro Val Lys Val Leu Lys Ala
385                 390                 395                 400

Pro Pro Ser Phe Lys Gly Ile Ser Gly Leu Gly Ala Gly His Ser Lys
                405                 410                 415
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Ala Thr Ile Gly Lys Val Asn Lys Ser Asn Ile Ala Ala Thr Pro Phe
            420                 425                 430

Ser Val Ala Asp Leu Gln Ala Ala Thr Asn Ser Phe Ser Gln Asp Asn
        435                 440                 445

Leu Ile Gly Glu Gly Ser Met Gly Arg Val Tyr Arg Ala Glu Phe Pro
    450                 455                 460

Asn Gly Gln Val Leu Ala Val Lys Lys Ile Asp Ser Ser Ala Ser Met
465                 470                 475                 480

Val Gln Asn Glu Asp Asp Phe Leu Ser Val Val Asp Ser Leu Ala Arg
                485                 490                 495

Leu Gln His Ala Asn Thr Ala Glu Leu Val Gly Tyr Cys Ile Glu His
            500                 505                 510

Asp Gln Arg Leu Leu Val Tyr Glu Tyr Val Ser Arg Gly Thr Leu Asn
        515                 520                 525

Glu Leu Leu His Phe Ser Gly Glu Asn Thr Lys Ala Leu Ser Trp Asn
    530                 535                 540

Val Arg Ile Lys Ile Ala Leu Gly Ser Ala Arg Ala Leu Glu Tyr Leu
545                 550                 555                 560

His Glu Val Cys Ala Pro Pro Val Val His His Asn Phe Lys Ser Ala
                565                 570                 575

Asn Ile Leu Leu Asp Asp Glu Leu Asn Pro His Val Ser Asp Cys Gly
            580                 585                 590

Leu Ala Ala Leu Ala Pro Ser Gly Ser Glu Arg Gln Val Ser Ala Gln
        595                 600                 605

Met Leu Gly Ser Phe Gly Tyr Ser Ala Pro Glu Tyr Ala Met Ser Gly
    610                 615                 620

Thr Tyr Thr Val Lys Ser Asp Val Tyr Ser Phe Gly Val Val Met Leu
625                 630                 635                 640

Glu Leu Leu Thr Gly Arg Lys Ser Leu Asp Ser Ser Arg Pro Arg Ser
                645                 650                 655

Glu Gln Ser Leu Val Arg Trp Ala Thr Pro Gln Leu His Asp Ile Asp
            660                 665                 670

Ala Leu Ala Arg Met Val Asp Pro Ser Leu Lys Gly Ile Tyr Pro Ala
        675                 680                 685

Lys Ser Leu Ser Arg Phe Ala Asp Ile Val Ala Leu Cys Val Gln Pro
    690                 695                 700

Glu Pro Glu Phe Arg Pro Pro Met Ser Glu Val Val Gln Ala Leu Val
705                 710                 715                 720

Arg Leu Met Gln Arg Ala Ser Leu Ser Lys Arg Arg Ser Glu Ser Ala
                725                 730                 735

Val Gly Ile Glu Ser Asn Glu Pro Ser Glu Thr Ser Leu
            740                 745


<210> SEQ ID NO 28
<211> LENGTH: 308
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 28

Met Ser Val Ser Gly Met Asp Asn Tyr Glu Lys Leu Glu Lys Val Gly
 1               5                  10                  15

Glu Gly Thr Tyr Gly Lys Val Tyr Lys Ala Arg Asp Lys Arg Ser Gly
            20                  25                  30

Gln Leu Val Ala Leu Lys Lys Thr Arg Leu Glu Met Glu Glu Glu Gly
        35                  40                  45
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Val Pro Ser Thr Ala Leu Arg Glu Val Ser Leu Leu Gln Met Leu Ser
    50                  55                  60

His Ser Met Tyr Ile Val Arg Leu Leu Cys Val Glu His Val Glu Lys
65                  70                  75                  80

Gly Ser Lys Pro Met Leu Tyr Leu Val Phe Glu Tyr Met Asp Thr Asp
                85                  90                  95

Leu Lys Lys Tyr Ile Asp Leu His Gly Arg Gly Pro Ser Gly Lys Pro
            100                 105                 110

Leu Pro Pro Lys Val Val Gln Ser Phe Met Tyr Gln Leu Cys Thr Gly
        115                 120                 125

Leu Ala His Cys His Gly His Gly Val Met His Arg Asp Leu Lys Pro
    130                 135                 140

Gln Asn Leu Leu Val Asp Lys Gln Thr Arg Arg Leu Lys Ile Ala Asp
145                 150                 155                 160

Leu Gly Leu Gly Arg Ala Phe Thr Val Pro Met Lys Ser Tyr Thr His
                165                 170                 175

Glu Ile Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gly Ala
            180                 185                 190

Thr His Tyr Ser Leu Pro Val Asp Ile Trp Ser Val Gly Cys Ile Phe
        195                 200                 205

Ala Glu Leu Val Arg Lys Met Pro Leu Phe Thr Gly Asp Ser Glu Leu
    210                 215                 220

Gln Gln Leu Leu His Ile Phe Arg Leu Leu Gly Thr Pro Asn Glu Thr
225                 230                 235                 240

Ile Trp Pro Gly Val Ser Gln His Arg Asp Trp His Glu Phe Pro Gln
                245                 250                 255

Trp Arg Pro Gln Asp Leu Ser Leu Ala Val Pro Gly Leu Ser Ala Val
            260                 265                 270

Gly Leu Asp Leu Leu Ala Lys Met Leu Val Phe Glu Pro Ser Lys Arg
        275                 280                 285

Ile Ser Ala Lys Ala Ala Leu Ser His Thr Tyr Phe Ala Asp Val Asp
    290                 295                 300

Lys Thr Ala Thr
305


<210> SEQ ID NO 29
<211> LENGTH: 425
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 29

Met Ala Asp Ala Lys Glu Glu Leu Ala Leu Arg Thr Glu Met His Trp
 1               5                  10                  15

Ala Val Arg Ser Asn Asp Val Gly Leu Leu Arg Thr Ile Leu Lys Lys
            20                  25                  30

Asp Lys Gln Leu Val Asn Ala Ala Asp Tyr Asp Lys Arg Thr Pro Leu
        35                  40                  45

His Ile Ala Ala Ser Leu Asp Cys Val Pro Val Ala Lys Val Leu Leu
    50                  55                  60

Ala Glu Gly Ala Glu Leu Asn Ala Lys Asp Arg Trp Gly Lys Ser Pro
65                  70                  75                  80

Arg Gly Glu Ala Glu Ser Ala Gly Tyr Met Glu Met Val Lys Leu Leu
                85                  90                  95

Lys Asp Tyr Gly Ala Glu Ser His Ala Gly Ala Pro Arg Gly His Val
            100                 105                 110
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Glu Ser Leu Ile Gln Val Ala Pro Pro Leu Pro Ser Asn Arg Asp Trp
        115                 120                 125

Glu Ile Ala Pro Ser Glu Ile Glu Leu Asp Thr Ser Glu Leu Ile Gly
    130                 135                 140

Lys Gly Ala Phe Gly Glu Ile Arg Lys Ala Leu Trp Arg Gly Thr Pro
145                 150                 155                 160

Val Ala Val Lys Thr Ile Arg Pro Ser Leu Ser Asn Asp Arg Met Val
                165                 170                 175

Ile Lys Asp Phe Gln His Glu Val Gln Leu Leu Val Lys Val Arg His
            180                 185                 190

Pro Asn Ile Val Gln Phe Leu Gly Ala Val Thr Arg Gln Arg Pro Leu
        195                 200                 205

Met Leu Val Thr Glu Phe Leu Ala Gly Gly Asp Leu His Gln Leu Leu
    210                 215                 220

Arg Ser Asn Pro Asn Leu Ala Pro Asp Arg Ile Val Lys Tyr Ala Leu
225                 230                 235                 240

Asp Ile Ala Arg Gly Met Ser Tyr Leu His Asn Arg Ser Lys Pro Ile
                245                 250                 255

Ile His Arg Asp Leu Lys Pro Arg Asn Ile Ile Val Asp Glu Glu His
            260                 265                 270

Glu Leu Lys Val Gly Asp Phe Gly Leu Ser Lys Leu Ile Asp Val Lys
        275                 280                 285

Leu Met His Asp Val Tyr Lys Met Thr Gly Gly Thr Gly Ser Tyr Arg
    290                 295                 300

Tyr Met Ala Pro Glu Val Phe Glu His Gln Pro Tyr Asp Lys Ser Val
305                 310                 315                 320

Asp Val Phe Ser Phe Gly Met Ile Leu Tyr Glu Met Phe Glu Gly Val
                325                 330                 335

Ala Pro Phe Glu Asp Lys Asp Ala Tyr Asp Ala Ala Thr Leu Val Ala
            340                 345                 350

Arg Asp Asp Lys Arg Pro Glu Met Arg Ala Gln Thr Tyr Pro Pro Gln
        355                 360                 365

Met Lys Ala Leu Ile Glu Asp Cys Trp Ser Pro Tyr Thr Pro Lys Arg
    370                 375                 380

Pro Pro Phe Val Glu Ile Val Lys Lys Leu Glu Val Met Tyr Glu Asp
385                 390                 395                 400

Cys Leu Leu Arg Leu Pro Lys Asp Arg Arg His Leu Arg Asp Ile Leu
                405                 410                 415

His Leu Arg Arg Asn Pro Ala Asp Ser
            420                 425


<210> SEQ ID NO 30
<211> LENGTH: 283
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 30

Met Lys Arg Tyr Gln Arg Arg Lys Val Gln Arg Leu Gly Arg Glu Gly
 1               5                  10                  15

Gln Val Leu Leu Glu Arg Thr Leu Phe Lys Gln Leu Arg Pro Ser Pro
            20                  25                  30

Phe Val Pro His Leu Leu Ala Thr Pro Ile Asp Ser Asp Asn Val Ala
        35                  40                  45

Leu Val Leu Asn Cys Val Leu Ala Gly Pro Leu Glu Leu Leu Leu Arg
    50                  55                  60
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Ser Pro Leu Asp Glu Asn Ser Ala Arg Phe Leu Val Ala Asn Val Val
65                  70                  75                  80

Leu Ala Val Glu Leu Leu His Lys Asp Gly Val Val Tyr Arg Gly Ile
                85                  90                  95

Ser Pro Asp Val Leu Met Ile Asp Arg Lys Gly Arg Leu Gln Leu Val
            100                 105                 110

Asp Phe Arg Phe Ala Lys Gln Met Ser Asp Glu Arg Thr Phe Thr Val
        115                 120                 125

Cys Gly Met Ala Asp Phe Leu Ala Pro Glu Ile Ile Gln Gly Gln Gly
    130                 135                 140

His Gly Leu Ala Ser Asp Trp Trp Ala Val Gly Val Leu Met Tyr Phe
145                 150                 155                 160

Met Leu Gln Thr Glu Leu Pro Phe Gly Ser Trp Arg Asp Asn Glu Leu
                165                 170                 175

Glu Ile Phe Gly Arg Ile Ala Arg Arg Gln Leu Thr Phe Pro Ser Ser
            180                 185                 190

Phe Ser Pro Glu Ala Val Asp Leu Ile Asp Lys Leu Leu Val Val Asp
        195                 200                 205

Pro Thr Lys Arg Leu Gly Cys Asp Ser His Gly Ser Leu Ala Ile Arg
    210                 215                 220

Glu His Pro Trp Phe Arg Gly Ile Asn Trp Asp Lys His Leu Asp Cys
225                 230                 235                 240

Ser Val Glu Val Pro Ser Glu Ile Met Thr Arg Leu Gln Leu Ala Ile
                245                 250                 255

Asp Phe Leu Pro Val Asp Asp Ser Tyr Gln Val Phe Asp Leu Gln Pro
            260                 265                 270

Asp Glu Asp Asp Pro Pro Trp Leu Asp Gly Trp
        275                 280


<210> SEQ ID NO 31
<211> LENGTH: 417
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 31

Met Asp Leu Gly Gly Asp Arg Met Arg Ala Pro Gln Arg Gln Ser Arg
 1               5                  10                  15

Glu Tyr Gln Tyr Arg Ser Leu Asp Val Phe Thr Glu Gln His Glu Gln
            20                  25                  30

Leu Gln Lys Gln Gln Gln Gln Asp Glu Tyr Gln Arg Thr Glu Leu Lys
        35                  40                  45

Leu Glu Thr Leu Pro Lys Met Leu Ser Asn Ala Thr Val Ser Ser Ser
    50                  55                  60

Pro Arg Ser Ser Pro Asp Gly Arg Arg Leu Arg Thr Val Ala Asn Lys
65                  70                  75                  80

Tyr Ala Val Glu Gly Met Val Gly Ser Gly Ala Phe Cys Lys Val Tyr
                85                  90                  95

Gln Gly Ser Asp Leu Thr Asn His Glu Val Val Gly Ile Lys Leu Glu
            100                 105                 110

Asp Thr Arg Thr Glu His Ala Gln Leu Met His Glu Ser Arg Leu Tyr
        115                 120                 125

Asn Ile Leu Arg Gly Gly Lys Gly Val Pro Asn Met Arg Trp Phe Gly
    130                 135                 140

Lys Glu Gln Asp Tyr Asn Val Met Val Leu Asp Leu Leu Gly Pro Asn
145                 150                 155                 160
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-continued

```
Leu Leu His Leu Phe Lys Val Cys Gly Leu Arg Phe Ser Leu Lys Thr
                165                 170                 175

Val Ile Met Leu Gly Tyr Gln Met Ile Asp Arg Val Glu Tyr Val His
            180                 185                 190

Ser Arg Gly Leu Val His Arg Asp Leu Lys Pro Asp Asn Phe Leu Met
        195                 200                 205

Gly Cys Gly Arg Gln Gly Asn Gln Val Phe Ile Ile Asp Phe Gly Leu
    210                 215                 220

Ala Lys Glu Tyr Met Asp Pro Ala Thr Arg Arg His Ile Pro Tyr Arg
225                 230                 235                 240

Asp Arg Lys Ser Phe Thr Gly Thr Ala Arg Tyr Ala Ser Arg Asn Gln
                245                 250                 255

His Arg Gly Ile Glu His Ser Arg Arg Asp Asp Ile Glu Ser Leu Gly
            260                 265                 270

Tyr Ile Leu Met Tyr Phe Leu Arg Gly Asn Leu Pro Trp Gln Gly Lys
        275                 280                 285

Gly Gly Gln Arg Leu Thr Asp Gln Lys Gln His Glu Tyr Met His Asn
    290                 295                 300

Lys Ile Lys Met Asn Thr Thr Val Glu Glu Leu Cys Asp Gly Tyr Pro
305                 310                 315                 320

Ser Gln Phe Ala Asp Phe Leu His His Ala Arg Ser Leu Gly Phe Tyr
                325                 330                 335

Glu Gln Pro Asp Tyr Cys Tyr Leu Arg Ser Leu Phe Arg Asp Leu Phe
            340                 345                 350

Ile Gln Lys Lys Phe Gln Leu Asp His Val Tyr Asp Trp Thr Val Tyr
        355                 360                 365

Thr Gln Leu Pro Gln Asn Gly Ser Leu Gln Ser Val Arg Ser Gln Asn
    370                 375                 380

Ser Ala Ala Ser Ser His Leu Gln Asn Arg Pro Ser Asn Val Ser Tyr
385                 390                 395                 400

Cys Pro Pro Leu Thr Lys Ser Glu Phe Arg Arg Glu Val Val Ala Ala
                405                 410                 415

Asn
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<210> SEQ ID NO 32
<211> LENGTH: 484
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 32

```
Met Glu Pro Arg Val Gly Asn Lys Tyr Arg Leu Gly Arg Lys Ile Gly
 1               5                  10                  15

Ser Gly Ser Phe Gly Glu Ile Tyr Leu Gly Thr Asn Val Gln Thr Asn
            20                  25                  30

Glu Glu Val Gly Ile Lys Leu Glu Ser Ile Lys Thr Lys His Pro Gln
        35                  40                  45

Leu Leu Tyr Glu Ser Lys Leu Tyr Arg Ile Leu Gln Gly Gly Thr Gly
    50                  55                  60

Ile Pro Asn Ile Arg Trp Phe Gly Ile Glu Gly Asp Tyr Asn Val Leu
65                  70                  75                  80

Val Leu Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys
                85                  90                  95

Ser Arg Lys Phe Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Leu
            100                 105                 110

Ile Asn Arg Val Glu Tyr Val His Ala Lys Ser Phe Leu His Arg Asp
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        115                 120                 125

Ile Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Arg Arg Ala Asn Gln
    130                 135                 140

Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Ser
145                 150                 155                 160

Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
                165                 170                 175

Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
            180                 185                 190

Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Leu Arg
        195                 200                 205

Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Gly Thr Lys Lys Gln Lys
    210                 215                 220

Tyr Glu Lys Ile Ser Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
225                 230                 235                 240

Cys Lys Asn Tyr Pro Ser Glu Phe Ala Ser Tyr Phe His Tyr Cys Arg
                245                 250                 255

Ser Leu Arg Phe Asp Asp Lys Pro Asp Tyr Ala Tyr Leu Lys Arg Ile
            260                 265                 270

Phe Arg Asp Leu Phe Ile Arg Glu Gly Phe Gln Phe Asp Tyr Val Phe
        275                 280                 285

Asp Trp Thr Ile Leu Lys Tyr Gln Gln Ser Gln Ile Ser Gly Gly Ser
    290                 295                 300

Ser Thr Arg Leu Gly Ala Ser Ala Gly Gln Thr Ser Gly Ala Leu Gly
305                 310                 315                 320

Thr Gly Ala Thr Gly Ser Arg Asp Leu Gln Arg Pro Thr Glu Pro Met
                325                 330                 335

Asp Pro Ser Arg Arg Arg Leu Pro Gly Gly Ala Asn Gly Ser Gly Val
            340                 345                 350

Ala Asn Ala Leu Asp Ser Ser Lys His Lys Ser Pro Gly Leu Asp Glu
        355                 360                 365

Ser Ala Lys Asp Ser Ala Leu Ala Val Val Ser Glu Pro Glu Arg Met
    370                 375                 380

His Thr Ser Ser Tyr Ala Thr Arg Gly Gly Ser Ser Ser Arg Arg Ala
385                 390                 395                 400

Val Leu Ser Ser Ser Arg Pro Ser Gly Ala Ser Ala Glu Val Val Asp
                405                 410                 415

Ser Ser Arg Thr Gly Ser Ser Lys Leu Gly Pro Thr Ser Leu Arg Ser
            420                 425                 430

Ser Ala Gly Met Gln Arg Ser Ser Pro Val Thr Ser Asp Pro Lys Arg
        435                 440                 445

Ile Ser Ser Arg His Pro Gln Pro Pro Ser Ala Asn Leu Arg Ile Tyr
    450                 455                 460

Glu Ala Ala Ile Lys Gly Val Glu Ser Leu Ser Val Glu Val Asp Gln
465                 470                 475                 480

Ser Arg Tyr Lys
```

<210> SEQ ID NO 33
<211> LENGTH: 333
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 33

```
Met Ser Lys Ala Arg Val Tyr Thr Asp Val Asn Val Gln Arg Pro Lys
 1               5                  10                  15
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```
Asp Tyr Trp Asp Tyr Glu Ala Leu Thr Val Gln Trp Gly Asp Gln Asp
            20                  25                  30

Asp Tyr Glu Val Val Arg Lys Val Gly Arg Gly Lys Tyr Ser Glu Val
        35                  40                  45

Phe Glu Gly Val Asn Ala Val Asn Ser Glu Arg Cys Val Met Lys Ile
    50                  55                  60

Leu Lys Pro Val Lys Lys Lys Lys Ile Lys Arg Glu Ile Lys Ile Leu
65                  70                  75                  80

Gln Asn Leu Cys Gly Gly Pro Asn Ile Val Lys Leu Leu Asp Ile Val
                85                  90                  95

Arg Asp Gln Gln Ser Lys Thr Pro Ser Leu Ile Phe Glu Tyr Val Asn
            100                 105                 110

Asn Thr Asp Phe Lys Val Leu Tyr Pro Thr Leu Thr Asp Phe Asp Ile
        115                 120                 125

Arg Tyr Tyr Ile His Glu Leu Leu Lys Ala Leu Asp Tyr Cys His Ser
    130                 135                 140

Gln Gly Ile Met His Arg Asp Val Lys Pro His Asn Val Met Ile Asp
145                 150                 155                 160

His Glu Gln Arg Lys Leu Arg Leu Ile Asp Trp Gly Leu Ala Glu Phe
                165                 170                 175

Tyr His Pro Gly Lys Glu Tyr Asn Val Arg Val Ala Ser Arg Tyr Phe
            180                 185                 190

Lys Gly Pro Glu Leu Leu Val Asp Leu Gln Asp Tyr Asp Tyr Ser Leu
        195                 200                 205

Asp Met Trp Ser Leu Gly Cys Met Phe Ala Gly Met Ile Phe Arg Lys
    210                 215                 220

Glu Pro Phe Phe Tyr Gly His Asp Asn Tyr Asp Gln Leu Val Lys Ile
225                 230                 235                 240

Ala Lys Val Leu Gly Thr Asp Glu Leu Asn Ser Tyr Leu Asn Lys Tyr
                245                 250                 255

Arg Leu Glu Leu Asp Pro His Leu Glu Ala Leu Val Gly Arg His Ser
            260                 265                 270

Arg Lys Pro Trp Ser Lys Phe Ile Asn Ala Asp Asn Gln Arg Leu Val
        275                 280                 285

Val Pro Glu Ala Val Asp Phe Leu Asp Lys Leu Leu Arg Tyr Asp His
    290                 295                 300

Gln Asp Arg Leu Thr Ala Lys Glu Ala Met Ala His Pro Tyr Phe Tyr
305                 310                 315                 320

Pro Val Lys Val Ser Glu Val Ser Asn Arg Arg Ser Ala
                325                 330


<210> SEQ ID NO 34
<211> LENGTH: 375
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 34

Met Glu Thr Ser Ser Gly Thr Pro Glu Leu Lys Val Ile Ser Thr Pro
 1               5                  10                  15

Thr Tyr Gly Gly His Tyr Val Lys Tyr Val Val Ala Gly Thr Asp Phe
            20                  25                  30

Glu Val Thr Ala Arg Tyr Lys Pro Pro Leu Arg Pro Ile Gly Arg Gly
        35                  40                  45

Ala Tyr Gly Ile Val Cys Ser Leu Phe Asp Thr Val Thr Gly Glu Glu
    50                  55                  60
```

-continued

```
Val Ala Val Lys Lys Ile Gly Asn Ala Phe Asp Asn Arg Ile Asp Ala
65                  70                  75                  80

Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu Arg His Met Asp His Glu
                85                  90                  95

Asn Val Val Ala Ile Thr Asp Ile Ile Arg Pro Pro Thr Arg Glu Asn
            100                 105                 110

Phe Asn Asp Val Tyr Ile Val Tyr Glu Leu Met Asp Thr Asp Leu His
        115                 120                 125

Gln Ile Ile Arg Ser Asn Gln Ala Leu Thr Glu Asp His Cys Gln Tyr
    130                 135                 140

Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn
145                 150                 155                 160

Val Leu His Arg Asp Leu Lys Pro Thr Asn Leu Leu Val Asn Ala Asn
                165                 170                 175

Cys Asp Leu Lys Ile Ala Asp Phe Gly Leu Ala Arg Thr Leu Ser Glu
            180                 185                 190

Thr Asp Phe Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro
        195                 200                 205

Glu Leu Leu Leu Asn Cys Ser Ala Tyr Thr Ala Ala Ile Asp Ile Trp
    210                 215                 220

Ser Val Gly Cys Ile Phe Met Glu Leu Leu Asn Arg Ser Ala Leu Phe
225                 230                 235                 240

Pro Gly Arg Asp Tyr Val His Gln Leu Arg Leu Ile Thr Glu Leu Ile
                245                 250                 255

Gly Thr Pro Glu Asp Arg Asp Leu Gly Phe Leu Arg Ser Asp Asn Ala
            260                 265                 270

Arg Arg Tyr Ile Lys His Leu Pro Arg Gln Ser Pro Ile Pro Leu Thr
        275                 280                 285

Gln Lys Phe Arg Gly Ile Asn Arg Ser Ala Leu Asp Leu Val Glu Lys
    290                 295                 300

Met Leu Val Phe Asp Pro Ala Lys Arg Ile Thr Val Glu Ala Ala Leu
305                 310                 315                 320

Ala His Pro Tyr Leu Ala Ser Leu His Asp Ile Asn Asp Glu Pro Ala
                325                 330                 335

Ser Val Ser Pro Phe Glu Phe Asp Phe Glu Glu Pro Pro Ile Ser Glu
            340                 345                 350

Glu His Ile Lys Asp Leu Ile Trp Arg Glu Ala Leu Asp Cys Ser Leu
        355                 360                 365

Gly Pro Asp Asp Met Val Gln
    370                 375


<210> SEQ ID NO 35
<211> LENGTH: 331
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 35

Met Gly Leu Thr Pro Phe Ser Cys Val Thr Val Gln Gly Tyr Val Arg
 1               5                  10                  15

Val Val Tyr Pro Asp Gly His Val Glu Asn Leu Ser Lys Ser Cys Ser
            20                  25                  30

Val His Asp Leu Leu Leu Gly Asn Pro Asp Tyr Tyr Val Cys Gly Ser
        35                  40                  45

Thr Pro Tyr Thr Ile Thr Asn Arg Met Ala Ala Glu Glu Val Leu Glu
    50                  55                  60
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```
Tyr Gly Val Thr Tyr Phe Val Cys Ala Thr Pro Asn Ala Gln Pro Phe
65                  70                  75                  80

Leu Glu Arg Gln Pro Lys Val Val His Arg Gly Ser Lys Ile Leu Pro
                85                  90                  95

Arg Phe Ser Lys His Gly Val His Val Arg Glu Leu Arg Ser Pro Thr
            100                 105                 110

His Gly Ser Gln Gln Ser Arg Lys Val Phe Asp Tyr His Ser Val Thr
        115                 120                 125

Met Gln Gln Leu Glu Ser Ile Arg Asn Glu Gly Pro Glu Pro His Leu
    130                 135                 140

Ala Gly Asp Arg Pro Ser Lys His Leu Lys Leu Val Phe Ile Arg His
145                 150                 155                 160

Cys Leu Arg Ala Leu Arg Leu Pro Arg Ile Ser Ile Asp Leu Met Glu
                165                 170                 175

Ser Pro Leu Pro Asn Leu Ser Gly Glu Ala Leu Ser Pro Thr Ala Thr
            180                 185                 190

Ala Lys Asp Glu Ile Thr Gln Met Ile Leu Lys Ser Ala Ala Arg Ser
        195                 200                 205

Glu Leu Gly Met Tyr Val Ser Lys Arg Gln Glu Phe Tyr Leu Arg Arg
    210                 215                 220

Ala Arg Arg Arg Arg Lys Phe Ala Trp Lys Pro Val Leu Gln Ser Ile
225                 230                 235                 240

Ser Glu Met Lys Pro Val Met Glu Phe His Thr Pro Met Ala Tyr Arg
                245                 250                 255

Asp Ser Gly Ser Pro Pro Lys Asn Ala Ser Thr Pro Ser Leu Pro Gly
            260                 265                 270

Pro Lys Asn Ile Ser Pro Pro Arg Gln Val Ser Val Pro Gln Arg Ser
        275                 280                 285

Ser Pro Pro Pro Lys Asn Val Ser Pro Pro Pro Gln Pro Ala Phe Val
    290                 295                 300

Ala Arg Thr Ala Ser Lys Tyr Ser Ala Ala Ser Gln Gln Val Gln Arg
305                 310                 315                 320

Asn Arg Gly Asn Ala Lys Ser Leu Tyr Met Ala
                325                 330


<210> SEQ ID NO 36
<211> LENGTH: 346
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 36

Met Ser Arg Arg Val Arg Arg Gly Gly Leu Arg Val Ala Val Pro Lys
 1               5                  10                  15

Gln Glu Thr Pro Val Ser Lys Phe Leu Thr Ala Ser Gly Thr Phe Gln
            20                  25                  30

Asp Asp Asp Ile Lys Leu Asn His Thr Gly Leu Arg Val Val Ser Ser
        35                  40                  45

Glu Pro Asn Leu Pro Thr Gln Thr Gln Ser Ser Ser Pro Asp Gly Gln
    50                  55                  60

Leu Ser Ile Ala Asp Leu Glu Leu Val Arg Phe Leu Gly Lys Gly Ala
65                  70                  75                  80

Gly Gly Thr Val Gln Leu Val Arg His Lys Trp Thr Asn Val Asn Tyr
                85                  90                  95

Ala Leu Lys Ala Ile Gln Met Asn Ile Asn Glu Thr Val Arg Lys Gln
            100                 105                 110
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-continued

```
Ile Val Gln Glu Leu Lys Ile Asn Gln Val Thr His Gln Gln Cys Pro
        115                 120                 125

Tyr Ile Val Glu Cys Phe His Ser Phe Tyr His Asn Gly Val Ile Ser
    130                 135                 140

Met Ile Leu Glu Tyr Met Asp Arg Gly Ser Leu Ser Asp Ile Ile Lys
145                 150                 155                 160

Gln Gln Lys Gln Ile Pro Glu Pro Tyr Leu Ala Val Ile Ala Ser Gln
                165                 170                 175

Val Leu Lys Gly Leu Glu Tyr Leu His Gln Val Arg His Ile Ile His
            180                 185                 190

Arg Asp Ile Lys Pro Ser Asn Leu Leu Ile Asn His Lys Gly Glu Val
        195                 200                 205

Lys Ile Ser Asp Phe Gly Val Ser Ala Val Leu Val His Ser Leu Ala
    210                 215                 220

Gln Arg Asp Thr Phe Val Gly Thr Cys Thr Tyr Met Ser Pro Glu Arg
225                 230                 235                 240

Leu Gln Gly Arg Ser Tyr Ala Tyr Asp Ser Asp Leu Trp Ser Leu Gly
                245                 250                 255

Leu Thr Leu Leu Glu Cys Ala Leu Gly Thr Phe Pro Tyr Lys Pro Ala
            260                 265                 270

Gly Met Glu Glu Gly Trp Gln Asn Phe Phe Ile Leu Met Glu Cys Ile
        275                 280                 285

Val Asn Gln Pro Pro Ala Ala Ala Ser Pro Asp Lys Phe Ser Pro Glu
    290                 295                 300

Phe Cys Ser Phe Ile Glu Ser Cys Ile Arg Lys Cys Pro Ser Glu Arg
305                 310                 315                 320

Pro Ser Thr Thr Asp Leu Leu Lys His Pro Phe Leu Gln Lys Tyr Asn
                325                 330                 335

Glu Glu Glu Tyr His Leu Ser Lys Ile Leu
            340                 345


<210> SEQ ID NO 37
<211> LENGTH: 346
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 37

Met Ser Arg Arg Val Arg Arg Gly Gly Leu Arg Val Ala Val Pro Lys
 1               5                  10                  15

Gln Glu Thr Pro Val Ser Lys Phe Leu Thr Ala Ser Gly Thr Phe Gln
            20                  25                  30

Asp Asp Asp Ile Lys Leu Asn His Thr Gly Leu Arg Val Val Ser Ser
        35                  40                  45

Glu Pro Asn Leu Pro Thr Gln Thr Gln Ser Ser Ser Pro Asp Gly Gln
    50                  55                  60

Leu Ser Ile Ala Asp Leu Glu Leu Val Arg Phe Leu Gly Lys Gly Ala
65                  70                  75                  80

Gly Gly Thr Val Gln Leu Val Arg His Lys Trp Thr Asn Val Asn Tyr
                85                  90                  95

Ala Leu Lys Ala Ile Gln Met Asn Ile Asn Glu Thr Val Arg Lys Gln
            100                 105                 110

Ile Val Gln Glu Leu Lys Ile Asn Gln Val Thr His Gln Gln Cys Pro
        115                 120                 125

Tyr Ile Val Glu Cys Phe His Ser Phe Tyr His Asn Gly Val Ile Ser
    130                 135                 140
```

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```
Met Ile Leu Glu Tyr Met Asp Arg Gly Ser Leu Ser Asp Ile Ile Lys
145                 150                 155                 160

Gln Gln Lys Gln Ile Pro Glu Pro Tyr Leu Ala Val Ile Ala Ser Gln
                165                 170                 175

Val Leu Lys Gly Leu Glu Tyr Leu His Gln Val Arg His Ile Ile His
            180                 185                 190

Arg Asp Ile Lys Pro Ser Asn Leu Leu Ile Asn His Lys Gly Glu Val
        195                 200                 205

Lys Ile Ser Asp Phe Gly Val Ser Ala Val Leu Val His Ser Leu Ala
    210                 215                 220

Gln Arg Asp Thr Phe Val Gly Thr Cys Thr Tyr Met Ser Pro Glu Arg
225                 230                 235                 240

Leu Gln Gly Arg Ser Tyr Ala Tyr Asp Ser Asp Leu Trp Ser Leu Gly
                245                 250                 255

Leu Thr Leu Leu Glu Cys Ala Leu Gly Thr Phe Pro Tyr Lys Pro Ala
            260                 265                 270

Gly Met Glu Glu Gly Trp Gln Asn Phe Phe Ile Leu Met Glu Cys Ile
        275                 280                 285

Val Asn Gln Pro Pro Ala Ala Ala Ser Pro Asp Lys Phe Ser Pro Glu
    290                 295                 300

Phe Cys Ser Phe Ile Glu Ser Cys Ile Arg Lys Cys Pro Ser Glu Arg
305                 310                 315                 320

Pro Ser Thr Thr Asp Leu Leu Lys His Pro Phe Leu Gln Lys Tyr Asn
                325                 330                 335

Glu Glu Glu Tyr His Leu Ser Lys Ile Leu
            340                 345


<210> SEQ ID NO 38
<211> LENGTH: 597
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 38

Met Gly Gln Cys Tyr Gly Lys Phe Asp Asp Gly Gly Glu Gly Glu Asp
 1               5                  10                  15

Leu Phe Glu Arg Gln Lys Val Gln Val Ser Arg Thr Pro Lys His Gly
            20                  25                  30

Ser Trp Ser Asn Ser Asn Arg Gly Ser Phe Asn Asn Gly Gly Gly Ala
        35                  40                  45

Ser Pro Met Arg Ala Lys Thr Ser Phe Gly Ser Ser His Pro Ser Pro
    50                  55                  60

Arg His Pro Ser Ala Ser Pro Leu Pro His Tyr Thr Ser Ser Pro Ala
65                  70                  75                  80

Pro Ser Thr Pro Arg Arg Asn Ile Phe Lys Arg Pro Phe Pro Pro Pro
                85                  90                  95

Ser Pro Ala Lys His Ile Gln Ser Ser Leu Val Lys Arg His Gly Ala
            100                 105                 110

Lys Pro Lys Glu Gly Gly Ala Ile Pro Glu Ala Val Asp Gly Glu Lys
        115                 120                 125

Pro Leu Asp Lys His Phe Gly Tyr His Lys Asn Phe Ala Thr Lys Tyr
    130                 135                 140

Glu Leu Gly His Glu Val Gly Arg Gly His Phe Gly His Thr Cys Tyr
145                 150                 155                 160

Ala Lys Val Arg Lys Gly Glu His Lys Gly Gln Ala Val Ala Val Lys
                165                 170                 175
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```
Ile Ile Ser Lys Ala Lys Met Thr Thr Ala Ile Ala Ile Glu Asp Val
            180                 185                 190

Gly Arg Glu Val Lys Ile Leu Lys Ala Leu Thr Gly His Gln Asn Leu
        195                 200                 205

Val Arg Phe Tyr Asp Ser Cys Glu Asp His Leu Asn Val Tyr Ile Val
    210                 215                 220

Met Glu Leu Cys Glu Gly Gly Glu Leu Leu Asp Arg Ile Leu Ser Arg
225                 230                 235                 240

Gly Gly Lys Tyr Ser Glu Glu Asp Ala Lys Val Val Val Arg Gln Ile
                245                 250                 255

Leu Ser Val Val Ala Phe Cys His Leu Gln Gly Val Val His Arg Asp
            260                 265                 270

Leu Lys Pro Glu Asn Phe Leu Phe Thr Thr Lys Asp Glu Tyr Ala Gln
        275                 280                 285

Leu Lys Ala Ile Asp Phe Gly Leu Ser Asp Phe Ile Lys Pro Asp Glu
    290                 295                 300

Arg Leu Asn Asp Ile Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val
305                 310                 315                 320

Leu His Arg Leu Tyr Ser Met Glu Ala Asp Val Trp Ser Ile Gly Val
                325                 330                 335

Ile Thr Tyr Ile Leu Leu Cys Gly Ser Arg Pro Phe Trp Ala Arg Thr
            340                 345                 350

Glu Ser Gly Ile Phe Arg Ala Val Leu Arg Ala Asp Pro Ser Phe Glu
        355                 360                 365

Glu Ala Pro Trp Pro Ser Ile Ser Pro Glu Ala Lys Asp Phe Val Lys
    370                 375                 380

Arg Leu Leu Asn Lys Asp Met Arg Lys Arg Met Thr Ala Ala Gln Ala
385                 390                 395                 400

Leu Thr His Pro Trp Ile Arg Ser Asn Asn Val Lys Ile Pro Leu Asp
                405                 410                 415

Ile Leu Val Tyr Arg Leu Val Arg Asn Tyr Leu Arg Ala Ser Ser Met
            420                 425                 430

Arg Lys Ala Ala Leu Lys Ala Leu Ser Lys Thr Leu Thr Glu Asp Glu
        435                 440                 445

Thr Phe Tyr Leu Arg Thr Gln Phe Met Leu Leu Glu Pro Ser Asn Asn
    450                 455                 460

Gly Arg Val Thr Phe Glu Asn Phe Arg Gln Ala Leu Leu Lys Asn Ser
465                 470                 475                 480

Thr Glu Ala Met Lys Glu Ser Arg Val Phe Glu Ile Leu Glu Ser Met
                485                 490                 495

Asp Gly Leu His Phe Lys Lys Met Asp Phe Ser Glu Phe Cys Ala Ala
            500                 505                 510

Ala Ile Ser Val Leu Gln Leu Glu Ala Thr Glu Arg Trp Glu Gln His
        515                 520                 525

Ala Arg Ala Ala Tyr Asp Ile Phe Glu Lys Glu Gly Asn Arg Val Ile
    530                 535                 540

Tyr Pro Asp Glu Leu Ala Lys Glu Met Gly Leu Ala Pro Asn Val Pro
545                 550                 555                 560

Ala Gln Val Phe Leu Asp Trp Ile Arg Gln Ser Asp Gly Arg Leu Ser
                565                 570                 575

Phe Thr Gly Phe Thr Lys Leu Leu His Gly Ile Ser Ser Arg Ala Ile
            580                 585                 590

Lys Asn Leu Gln Gln
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595

<210> SEQ ID NO 39
<211> LENGTH: 549
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 39

Met Gly Asn Thr Ser Ser Arg Gly Ser Arg Lys Ser Thr Arg Gln Val
1 5 10 15

Asn Gln Gly Val Gly Ser Gln Asp Thr Arg Glu Lys Asn Asp Ser Val
20 25 30

Asn Pro Lys Thr Arg Gln Gly Gly Ser Val Gly Ala Asn Asn Tyr Gly
35 40 45

Gly Lys Pro Ser Ser Gly Ala Gln Ala Gly Glu Arg Ser Thr Ser Ala
50 55 60

Pro Ala Ala Leu Pro Arg Pro Lys Pro Ala Ser Arg Ser Val Ser Gly
65 70 75 80

Val Leu Gly Lys Pro Leu Ser Asp Ile Arg Gln Ser Tyr Ile Leu Gly
85 90 95

Arg Glu Leu Gly Arg Gly Gln Phe Gly Val Thr Tyr Leu Cys Thr Asp
100 105 110

Lys Met Thr Asn Glu Ala Tyr Ala Cys Lys Ser Ile Ala Lys Arg Lys
115 120 125

Leu Thr Ser Lys Glu Asp Ile Glu Asp Val Lys Arg Glu Val Gln Ile
130 135 140

Met His His Leu Ser Gly Thr Pro Asn Ile Val Val Leu Lys Asp Val
145 150 155 160

Phe Glu Asp Lys His Ser Val His Leu Val Met Glu Leu Cys Ala Gly
165 170 175

Gly Glu Leu Phe Asp Arg Ile Ile Ala Lys Gly His Tyr Ser Glu Arg
180 185 190

Ala Ala Ala Asp Met Cys Arg Val Ile Val Asn Val Val His Arg Cys
195 200 205

His Ser Leu Gly Val Phe His Arg Asp Leu Lys Pro Glu Asn Phe Leu
210 215 220

Leu Ala Ser Lys Ala Glu Asp Ala Pro Leu Lys Ala Thr Asp Phe Gly
225 230 235 240

Leu Ser Thr Phe Phe Lys Pro Gly Asp Val Phe Gln Asp Ile Val Gly
245 250 255

Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu Lys Arg Ser Tyr Gly Pro
260 265 270

Glu Ala Asp Val Trp Ser Ala Gly Val Ile Val Tyr Ile Leu Leu Cys
275 280 285

Gly Val Pro Pro Phe Trp Ala Glu Thr Glu Gln Gly Ile Phe Asp Ala
290 295 300

Val Leu Lys Gly His Ile Asp Phe Glu Asn Asp Pro Trp Pro Lys Ile
305 310 315 320

Ser Asn Gly Ala Lys Asp Leu Val Arg Lys Met Leu Asn Pro Asn Val
325 330 335

Lys Ile Arg Leu Thr Ala Gln Gln Val Leu Asn His Pro Trp Met Lys
340 345 350

Glu Asp Gly Asp Ala Pro Asp Val Pro Leu Asp Asn Ala Val Leu Thr
355 360 365

Arg Leu Lys Asn Phe Ser Ala Ala Asn Lys Met Lys Lys Leu Ala Leu

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    370                 375                 380

Lys Val Ile Ala Glu Ser Leu Ser Glu Glu Glu Ile Val Gly Leu Arg
385                 390                 395                 400

Glu Met Phe Lys Ser Ile Asp Thr Asp Asn Ser Gly Thr Val Thr Phe
                405                 410                 415

Glu Glu Leu Lys Glu Gly Leu Leu Lys Gln Gly Ser Lys Leu Asn Glu
            420                 425                 430

Ser Asp Ile Arg Lys Leu Met Glu Ala Ala Asp Val Asp Gly Asn Gly
        435                 440                 445

Lys Ile Asp Phe Asn Glu Phe Ile Ser Ala Thr Met His Met Asn Lys
    450                 455                 460

Thr Glu Lys Glu Asp His Leu Trp Ala Ala Phe Met His Phe Asp Thr
465                 470                 475                 480

Asp Asn Ser Gly Tyr Ile Thr Ile Asp Glu Leu Gln Glu Ala Met Glu
                485                 490                 495

Lys Asn Gly Met Gly Asp Pro Glu Thr Ile Gln Glu Ile Ile Ser Glu
            500                 505                 510

Val Asp Thr Asp Asn Asp Gly Arg Ile Asp Tyr Asp Glu Phe Val Ala
        515                 520                 525

Met Met Arg Lys Gly Asn Pro Gly Ala Glu Asn Gly Gly Thr Val Asn
    530                 535                 540

Lys Pro Arg His Arg
545


<210> SEQ ID NO 40
<211> LENGTH: 18
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 40

caggaaacag ctatgacc                                                  18


<210> SEQ ID NO 41
<211> LENGTH: 19
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 41

ctaaagggaa caaaagctg                                                 19


<210> SEQ ID NO 42
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 42

tgtaaaacga cggccagt                                                  18


<210> SEQ ID NO 43
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 43
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ccacggtctt cggctgctgg tcgtg 25

<210> SEQ ID NO 44
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<400> SEQUENCE: 44

gcagcacagc accaccagcg gctat 25

<210> SEQ ID NO 45
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 45

gcgcccagtg agtagctcca gcatt 25

<210> SEQ ID NO 46
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<212> TYPE: DNA
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<400> SEQUENCE: 46

atcccgggtg agtatcactt acggtggcga 30

<210> SEQ ID NO 47
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 47

gcgttaactc gaccaaggtc actattccaa gca 33

<210> SEQ ID NO 48
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 48

cggtgcccac ctcgttcctg tggtt 25

<210> SEQ ID NO 49
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 49

atcccgggag tgggtggttg gactgtaagg a 31

<210> SEQ ID NO 50
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 50

gcgttaacct tcgtcttgga caggtagagg ttac 34

<210> SEQ ID NO 51
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 51

gactcagccc cgtaatcctt caaca 25

<210> SEQ ID NO 52
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 52

atcccgggca acgagaagca ttcgagatgg c 31

<210> SEQ ID NO 53
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 53

gcgttaacga gcatcacgat actcggtgat ttc 33

<210> SEQ ID NO 54
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 54

cgacggctaa taccacgttg gcgacca 27

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<211> LENGTH: 33
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<400> SEQUENCE: 55

atcccgggct gtgatgtcgg tgtggtgctc tgc 33

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 56

gcgagctcgc accactgaat gatggagact cagg 34

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<210> SEQ ID NO 57
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<400> SEQUENCE: 57

cgaccgcagc ccatgaggaa gttat 25

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<400> SEQUENCE: 58

atcccgggct cacgtagtgc actgaactct gtc 33

<210> SEQ ID NO 59
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<400> SEQUENCE: 59

gcgttaacat gcccatcttc tcatactcag acc 33

<210> SEQ ID NO 60
<211> LENGTH: 25
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ctcgcctacc aagccccatt agaaa 25

<210> SEQ ID NO 61
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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 61

atcccgggtt gtcgaggacg gagagagaag ag 32

<210> SEQ ID NO 62
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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 62

gcgttaacct taggaatcgt atggcagaga gct 33

<210> SEQ ID NO 63
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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 63

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gcttcacaat gttgggccct ccaca 25

<210> SEQ ID NO 64
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 64

gcgttaacgg gaggaaggtc gggggaagag acg 33

<210> SEQ ID NO 65
<211> LENGTH: 33
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 65

gcgagctcag cgcttcgcac aactgagaaa cct 33

<210> SEQ ID NO 66
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 66

acgagaaggt tggtgggctt caagt 25

<210> SEQ ID NO 67
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 67

atcccgggcg agccatggcg ccacttgctt 30

<210> SEQ ID NO 68
<211> LENGTH: 33
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 68

gcgttaacgc cgagcaacaa tgtctgctgg atg 33

<210> SEQ ID NO 69
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 69

cccggtaagc catcggagtg tggaa 25

<210> SEQ ID NO 70
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 70

atcccgggct tgtattggct cggataattt 30

<210> SEQ ID NO 71
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 71

gcgttaacgg caatatctgc acagccgttc act 33

<210> SEQ ID NO 72
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 72

gtgtctcgct gggccaagga atgaa 25

<210> SEQ ID NO 73
<211> LENGTH: 35
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 73

atcccgggcg gtcgagtcgt attaggtgtt gtttc 35

<210> SEQ ID NO 74
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 74

gagctccggt aggtccgacc tcttcaattg 30

<210> SEQ ID NO 75
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 75

gacgacgcga agcccggtgt ggttga 26

<210> SEQ ID NO 76
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 76

atcccgggag aggctgatct gatgctacag t 31

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<210> SEQ ID NO 77
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 77

atgagctctg gcggattggc gaggtagttc gac 33

<210> SEQ ID NO 78
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 78

cggcgcaacg tagtatgcgc ttcca 25

<210> SEQ ID NO 79
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 79

cgcggtgaac aacaccttgc aggtgac 27

<210> SEQ ID NO 80
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 80

gctcgggtca gccctcaaca ccgca 25

<210> SEQ ID NO 81
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 81

gttaaagctt gtgcagcagt catgc 25

<210> SEQ ID NO 82
<211> LENGTH: 31
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 82

atcccgggtg taggcgggcg aggttcgatg c 31

<210> SEQ ID NO 83
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 83

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gcgttaacga caaccggagt agaacggcag tcca 34

<210> SEQ ID NO 84
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 84

agaagcgagg aatgggcagg gacga 25

<210> SEQ ID NO 85
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 85

atcccgggcg aactgcgatc tgagattcca ac 32

<210> SEQ ID NO 86
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 86

gcgttaacga gatccaaccg aagccatcct acga 34

<210> SEQ ID NO 87
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 87

gcgctgcaga tttcatttgg agaggacacg 30

<210> SEQ ID NO 88
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 88

cgcggccggc ctcagaagaa ctcgtcaaga aggcg 35

<210> SEQ ID NO 89
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 89

gctgacacgc caagcctcgc tagtc 25

<210> SEQ ID NO 90
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 90

gcgttaactc gaccaaggtc actattccaa gca 33

<210> SEQ ID NO 91
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 91

gcgttaacct tcgtcttgga caggtagagg ttac 34

<210> SEQ ID NO 92
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 92

gcgttaacga gcatcacgat actcggtgat ttc 33

<210> SEQ ID NO 93
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 93

gcgagctcgc accactgaat gatggagact cagg 34

<210> SEQ ID NO 94
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 94

gcgttaacat gcccatcttc tcatactcag acc 33

<210> SEQ ID NO 95
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 95

gcgttaacct taggaatcgt atggcagaga gct 33

<210> SEQ ID NO 96
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 96

gcgagctcag cgcttcgcac aactgagaaa cct 33

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<210> SEQ ID NO 97
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 97

gcgttaacgg caatatctgc acagccgttc act 33

<210> SEQ ID NO 98
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 98

gcgttaacgg caatatctgc acagccgttc act 33

<210> SEQ ID NO 99
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 99

gagctccggt aggtccgacc tcttcaattg 30

<210> SEQ ID NO 100
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 100

atgagctctg gcggattggc gaggtagttc gac 33

<210> SEQ ID NO 101
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 101

gcgttaacga caaccggagt agaacggcag tcca 34

<210> SEQ ID NO 102
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 102

gcgttaacga gatccaaccg aagccatcct acga 34

<210> SEQ ID NO 103
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 103

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cccagtaata gcagggttgg aggaa 25

<210> SEQ ID NO 104
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 104

ggctgcctga agatccgcta cagag 25

<210> SEQ ID NO 105
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 105

cgtcaggcta ctttgcgtgg agcac 25

<210> SEQ ID NO 106
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 106

cggtgctggc taacaccagg ccaga 25

<210> SEQ ID NO 107
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 107

atcccgggca acgagaagca ttcgagatgg c 31

<210> SEQ ID NO 108
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 108

gcgttaacga gcatcacgat actcggtgat ttc 33

<210> SEQ ID NO 109
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 109

cgtggcatct ctcccgatgt tctta 25

<210> SEQ ID NO 110
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 110

ggccaactga aggcgtgtca tgatc 25

<210> SEQ ID NO 111
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 111

ctcgagggct cgttcaccgt gacct 25

<210> SEQ ID NO 112
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 112

cggaggtaac agtagtcagg ctgctc 26

<210> SEQ ID NO 113
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 113

ccgcgaccct tccacgcatc agcat 25

<210> SEQ ID NO 114
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 114

cctccaggaa gcctgcgccg agaag 25

<210> SEQ ID NO 115
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 115

ggacattgtc cgtgatcagc aatcga 26

<210> SEQ ID NO 116
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 116

cagcctctgg aacaaccaga cgctg 25

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<210> SEQ ID NO 117
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 117

gtcaccgcga ggtacaagcc accac 25

<210> SEQ ID NO 118
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 118

gcagctctgg agctctgtac cacct 25

<210> SEQ ID NO 119
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 119

acggccacgt cgagaatctg agcaa 25

<210> SEQ ID NO 120
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 120

cgaagtgctc gcaagcaatg ccgaa 25

<210> SEQ ID NO 121
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 121

atcccgggcg gtcgagtcgt attaggtgtt gtttc 35

<210> SEQ ID NO 122
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 122

gagctccggt aggtccgacc tcttcaattg 30

<210> SEQ ID NO 123
<211> LENGTH: 26

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 123

gggcaactgt caatagcaga cctgga 26

<210> SEQ ID NO 124
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 124

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The invention claimed is:

1. A transgenic plant cell transformed with an expression vector comprising an isolated polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence comprising nucleotides 1 to 2784 of SEQ ID NO:14; and

b) a polynucleotide encoding a polypeptide having a sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

2. The plant cell of claim **1**, wherein the polynucleotide has the sequence comprising nucleotides 1 to 2784 of SEQ ID NO:14.

3. The plant cell of claim **1**, wherein the polynucleotide encodes the polypeptide having the sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

4. A transgenic plant transformed with an expression cassette comprising an isolated polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence comprising nucleotides 1 to 2784 of SEQ ID NO14; and

b) a polynucleotide encoding a polypeptide having a sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

5. The plant of claim **4**, wherein the polynucleotide has the sequence comprising nucleotides 1 to 2784 of SEQ ID NO:14.

6. The plant of claim **4**, wherein the polynucleotide encodes the polypeptide having the sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

7. The plant of claim **4**, further described as a monocot.

8. The plant of claim **5**, further described as a dicot.

9. The plant of claim **4**, wherein the plant is selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, tagetes, potato, tobacco, eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix* species, oil palm, coconut, perennial grasses, and a forage crop plant.

10. The plant of claim **9**, which is maize.

11. The plant of claim **9**, which is soybean.

12. The plant of claim **9**, which is rapeseed or canola.

13. The plant of claim **9**, which is cotton.

14. A seed which is true breeding for a transgene comprising a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence comprising nucleotides 1 to 2784 of SEQ ID NO:14; and

b) a polynucleotide encoding a polypeptide having a sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

15. The seed of claim **14**, wherein the polynucleotide has the sequence comprising nucleotides 1 to 2784 of SEQ ID NO:14.

16. The seed of claim **14**, wherein the polynucleotide encodes the polypeptide having the sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

17. An isolated nucleic acid comprising a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence comprising nucleotides 1 to 2784 of SEQ ID NO:14; and

b) a polynucleotide encoding a polypeptide having a sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

18. The isolated nucleic acid of claim **17**, wherein the polynucleotide has the sequence comprising nucleotides 1 to 2784 of SEQ ID NO:14.

19. The isolated nucleic acid of claim **17**, wherein the polynucleotide encodes the polypeptide having the sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

20. A method of producing a drought-tolerant transgenic plant, the method comprising the steps of:

a) transforming a plant cell with an expression vector comprising a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence comprising nucleotides 1 to 2784 of SEQ ID NO:14; and

b) a polynucleotide encoding a polypeptide having a sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

21. The method of claim **20**, wherein the polynucleotide has the sequence comprising nucleotides 1 to 2784 of SEQ ID NO:14.

22. The method of claim **20**, wherein the polynucleotide encodes the polypeptide having the sequence comprising amino acids 1 to 749 of SEQ ID NO:27.

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